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OM protein - protein search, using sw model

Run on: April 7, 2004, 10:41:40 ; Search time 24 Seconds
(without alignments)
2019.866 Million cell updates/sec

Title: US-10-029-065-2

Perfect score: 4859

Sequence: 1 MNENLEQSKLPKLDKQ.....KMKTDLERDAVDSHWLQOFF 939

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pdp.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pdp.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pdp.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pdp.*
- 5: /cgn2_6/ptodata/2/iaa/PTCUS_COMB.pdp.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1841.5	37.9	934	1	US-08-457-176-2
2	1841.5	37.9	934	1	US-08-457-175-2
3	1841.5	37.9	934	3	US-08-709-784-1
4	1841.5	37.9	934	4	US-09-651-656-3
5	1841.5	37.9	934	4	US-09-650-855-3
6	1841.5	37.9	934	4	US-09-708-200-13
7	1841.5	37.9	934	4	US-09-788-657-19
8	1841.5	37.9	1010	4	US-09-512-250C-31
9	1841.5	37.4	935	4	US-09-512-250C-33
10	1761	36.2	940	4	US-09-512-250C-2
11	1571	32.3	1042	4	US-09-512-250C-32
12	797	16.4	891	4	US-09-134-001C-4913
13	740.5	15.2	819	4	US-09-651-656-15
14	740.5	15.2	819	4	US-09-650-855-15
15	724.5	14.9	240	4	US-09-651-656-1
16	724.5	14.9	240	4	US-09-650-855-1
17	720.5	14.8	858	4	US-09-134-000C-5428
18	719	14.8	885	4	US-09-107-532A-5104
19	715	14.7	855	2	US-08-468-558-2
20	715	14.7	855	3	US-08-676-444-2
21	708	14.6	1307	4	US-09-252-991A-20867
22	675.5	13.9	853	2	US-08-468-558-3
23	675.5	13.9	853	3	US-08-676-444-3
24	663	13.6	874	4	US-09-543-681A-6958
25	654	13.5	855	4	US-09-489-039A-10151
26	652	13.4	891	4	US-09-328-352-6637
27	646.5	13.3	793	2	US-08-468-558-5

Sequence 5, Appli
Sequence 22, Appl
Sequence 1012, Ap
Sequence 54, Appl
Sequence 29, Appl
Sequence 2, Appli
Sequence 27, Appl
Sequence 4386, Ap
Sequence 6734, Ap
Sequence 3866, Ap
Sequence 6056, Ap
Sequence 4217, Ap
Sequence 3903, Ap
Sequence 43, Appl
Sequence 43, Appl
Sequence 5, Appli
Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-08-457-176-2
; Sequence 2, Application US/08457176
; Patent No. 5591826
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: de la Chapelle, Albert
; TITLE OF INVENTION: Mutator Gene and Hereditary
; TITLE OF INVENTION: No. 5591826-Polypoid Colorectal Cancer
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie, and Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,176
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 530

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160295
; FILING DATE: 02-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.

REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.44900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202.508.9100
; TELEFAX: 202.508.9299

TELEX: 197430 BMB UT
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 934 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens

US-08-457-176-2

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Query Match      37.9%; Score 1841.5; DB 1; Length 934;
Best Local Similarity 43.0%; Pred. No. 1.8e-164;
Matches 403; Conservative 172; Mismatches 307; Indels 55; Gaps 19;

QY 14 LKLDKQAGGFLSPFKTLPKDP-RAVRLPDRDYVTSHGDDATFAETTYHTTALRQLG 72
Db 9 LQLESAAEVGFVRPFGQPEKPTTVRLPDRGDFYTAHGEDALLAAREVFKTQGVIKYMG 68

QY 73 NR-ADALSSVSVRNMFTIARDILLERMDRTLELYEGSGN-----WRLVKSSTPGN 124
Db 69 PAGAKNLQSVLSKMFESFVKDLLLVROYR-VEVYKRNAGKASKENDWYLAAYKASPGN 127

QY 125 LGSFEDILFANNEMONSPIVIAALAPNFGQNGCEVGLGYVDITKRVLGLTEFLDDSHFTNL 184
Db 128 LSQFEDILFGNNDMSASIGVGVKMSAVDQGVGVYVDSIQKLGCLCEFPDNDQFSNL 187

QY 185 ESALVALGCRECLVP-AET-GKSSEYRPMFDAISRCGVMTTERKTEFKGRDLVDLQRL 242
Db 188 EALLIQIGPKCEVLPFGGETAGDMGKLRIQI---IQRGGILLITERKKADFTKDIYQDLNRL 244

QY 243 VKG-----SVEPVRDLVSGFECASGALGCLISYAEILLADESNYGVYKQYNLSYM 294
Db 245 LKGGKGEQWNSAVLPME-----NQVAVSSLSAVIKFLELLSDSNFGQFELTTFDFSQYM 300

QY 295 RLDSAAAMRALNWE-SKSDANKNFSIFGLMNRCTCTAGMKRLHMLWKQPLLDVVEINCR 353
Db 301 KLDIAAVALNALNVEFQSGVEDTQSGSLAALNK-CKTPQGRVLNWNQIKOPLMDKRIEER 359

QY 354 LDVQSFEVDAALRODLOH-LKRISDIERLTHNLERKASLVHVVKLYQSSSTRVPIYKS 412
Db 360 LNLVAFVEDAEELRQLQEDLLRRPDLNRLAKKFORQAANLQDCVRLVQGINPNVQI 419

QY 413 VLERHDGQATLIRERYIDSLSEKSDNHLNFKFGLVETSVDLDQLENGEYMISSAYDPN 472
Db 420 ALERHEGKHQKLLAVFVPLTDLRSD--FSKFEQMIETTLDMQVENHEFLVKPSFSDN 477

QY 473 LSALDKDEQETLROHNLHKKQANDLDPIDKSLDKDKETQGHVPRITTKKEPKVRKQL 532
Db 478 LSELREIMNDLKKMOWSTLISAARDLGLDPGQKQLDSSAQFGYTPRVCKEKEVLNR-- 535

QY 533 NGHYIVLETRKGVKFTYTKLKLQDQFOKIVVEEYKSCQKELVARVVOATAASFSEVAGI 592
Db 536 KKNFSTVDIQKNGVKFTNSKLTSLNEEYTKNKTEVEEAQDAIVKEIVNITSSGVVPMQLT 595

QY 593 AGVLAELVDLLSPADLAASCPPTYPNISPDPDTGDIILEGCRHPCVBAQDWNSTPNDC 652
Db 596 NDVLAQLDAVSVFAHVSAGPVYVPAILEKGGGRILLKASHHACVQVQDEIAFPNDV 655

QY 653 RLVRGSEWFIITGPNMGKSTVIROGVNVLMAQVGSFVPCDNATISIDICIFARVAGAG 712
Db 656 YFEKDKQMFHIIITGPNMGKSTVIROGVNVLMAQVGSFVPCDNATISIDICIFARVAGAG 715

QY 713 DCQLRGVSTFMQEMLETSILKIGATDRSLIIDELGRGTSTYDGFGLAWAICEHIVVEIK 772
Db 716 DSQKLGKSTFMAEMLETSILRSATKDSLIIDELGRGTSTYDGFGLAWAISVIATKIG 775

QY 773 APTLPATHFHELTALANGDNCHKKAGTIANPHVFAHIDPNSRKLTMLYKVPHPGACDOS 832
Db 776 AFCWFATHELTALAN-----QIPTVNNLHVTAL--TTEETLTMLYQVKKVGCDS 825

QY 833 FGHVAFEFANFPSSVVALAREKASELEDFSPIALIPN-DIKEAASKR--KREFDRHDVS 888
Db 826 FGHVAFELANFPKPVIECAKQALEEFOYIGESQGYDINEPAAKKYLERE----- 878

QY 889 RGTARARQFLQDFAQLPDLKMDPNVVRQKLSKMKTDL 925
Db 879 QGEKIIQEFLSKVKQMPFTESEENITIKLQKLAEV 915

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RESULT 2
 US-08-457-175-2
 ; Sequence 2, Application US/08457175

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; Patent No. 5693470
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: de la Chapelle, Albert
; TITLE OF INVENTION: Mutator Gene and Hereditary
; TITLE OF INVENTION: No. 5693470-Polyposis Colorectal Cancer
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie, and Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,175
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160295
; FILING DATE: 02-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.44900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202.508.9100
; TELEFAX: 202.508.9299
; TELEX: 197430 BMB UT
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 934 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-457-175-2

Query Match      37.9%; Score 1841.5; DB 1; Length 934;
Best Local Similarity 43.0%; Pred. No. 1.8e-164;
Matches 403; Conservative 172; Mismatches 307; Indels 55; Gaps 19;

QY 14 LKLDKQAGGFLSPFKTLPKDP-RAVRLPDRDYVTSHGDDATFAETTYHTTALRQLG 72
Db 9 LQLESAAEVGFVRPFGQPEKPTTVRLPDRGDFYTAHGEDALLAAREVFKTQGVIKYMG 68

QY 73 NR-ADALSSVSVRNMFTIARDILLERMDRTLELYEGSGN-----WRLVKSSTPGN 124
Db 69 PAGAKNLQSVLSKMFESFVKDLLLVROYR-VEVYKRNAGKASKENDWYLAAYKASPGN 127

QY 125 LGSFEDILFANNEMONSPIVIAALAPNFGQNGCEVGLGYVDITKRVLGLTEFLDDSHFTNL 184
Db 128 LSQFEDILFGNNDMSASIGVGVKMSAVDQGVGVYVDSIQKLGCLCEFPDNDQFSNL 187

QY 185 ESALVALGCRECLVP-AET-GKSSEYRPMFDAISRCGVMTTERKTEFKGRDLVDLQRL 242
Db 188 EALLIQIGPKCEVLPFGGETAGDMGKLRIQI---IQRGGILLITERKKADFTKDIYQDLNRL 244

QY 243 VKG-----SVEPVRDLVSGFECASGALGCLISYAEILLADESNYGVYKQYNLSYM 294
Db 245 LKGGKGEQWNSAVLPME-----NQVAVSSLSAVIKFLELLSDSNFGQFELTTFDFSQYM 300

QY 295 RLDSAAAMRALNWE-SKSDANKNFSIFGLMNRCTCTAGMKRLHMLWKQPLLDVVEINCR 353

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Db 360 LNLVEAFVEDAELRQTLQEDLLRRFPDLNRLAKKFORQAANLQDCYRLYQGINQLPNVIQ 419
Qy 413 VLEHDCQFATLIRERYIDSLKESDDNHLNKFGLVETSDLDQLENGEYMISSAYDPN 472
Db 420 ALEKHGKHQKLLAVFVFTPLDRLSD--FSKQEMIEITLDMQOVENHFLVPSFDPN 477
Qy 473 LSALKDQEQETLERQIHNHLKQTANDLPLDKSLDKETQFGHVFRITKKEEKKVRKQL 532
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Qy 533 NSHYVILETRKQGVKFTYTKLKLQDQFOKIVEYKSCQKELVARVVOATAASFSEVAGI 592
Db 536 NKNFSTVDIQKNGVKFTNSKLTSLNEEYTKNKTETEYEAQDAIVKEIWNISSGYVPMQTL 595
Qy 593 AGVLAELDVLSPADLAASCFTPTVTRNISPDPDGTGDIILEGCRHPCVEAQDWNINSINDC 652
Db 596 NDVLAQLDAVSVFAHVSNGAPVVPVRAILEKGGQRIILKASRHACVEQDEIAFINDV 655
Qy 653 RLVRGESWFOITGPNMGKSTYIRQGVNVMAOVGSFVPCDNATISIRDCIFARYGAG 712
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Qy 713 DCQLRGVSTFQEMLETA SILKGTDRSLIIDLGRGTSTYDGFGLAWAICEHIVEIK 772
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Db 776 AFCMFATHFHETLAN-----QPTVNNLHVTA--TTEETLTMLYKVKGVCDDQS 825
Qy 833 FGIHVAEFANPPSVVALAKASELEDFSPAIIPN-DIKEAASKR---KREFDRHDVS 888
Db 826 FGIHVAELANFPKHVIECAKQKALEBEFQYIGESQGVIMEPAKKCYLERE----- 878
Qy 889 RGTARARQFLQDPAQLPLDKMDPNVVRQKLSKMTDL 925
Db 879 QGEKIIQEFKSVKQMPPTMSEENITIKLKQKAEV 915

RESULT 3

US-08-709-784-1
; Sequence 1, Application US/08709784
; Patent No. 6048701
; GENERAL INFORMATION:
; APPLICANT: The Johns Hopkins University
; TITLE OF INVENTION: Antibody Detection of Mismatch Repair
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESS: Banner & Allegretti, Ltd.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,784
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/480,351
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 1107.57434
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 934 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-709-784-1

Query Match 37.9%; Score 1841.5; DB 3; Length 934;
Best Local Similarity 43.0%; Pred. No. 1.8e-164;
Matches 403; Conservative 172; Mismatches 307; Indels 55; Gaps 19;
Qy 14 LKLDKAOAQGLSFFKLPKDP-RAVLEDFDRDYTTSHGDDATFIAETYYHTTTALRQLG 72
Db 9 LQLESAAEVGFVRFFQGMPEKPTTVLDFDRGDFYTAHGEDALLAAREVFKTGVIKMG 68
Qy 73 NR-ADALSSVSVSRNMPETIARDILLERMORTLELYGSGSN-----WRLVKSGETPGN 124
Db 69 PAGAKNLQSVLVSKMNPESFVKOLLVRQYR-VEVYKNRAGNKASKENDWYLAVKASPGN 127
Qy 125 LGSFEDILFANNQNSPVIATAALAPNFGQNGCEVGLGVVDITKVLGTETFLDDSHFTNL 184
Db 128 LSFEDILFNGNMSASIGVGVGMSAVDQQRQGVGVDSIQKLGICEPFDNDQSNL 187
Qy 185 ESALVALGCRECLVP-AET-GKSSEYRPMFDAISRCGVMMVTERKTKTFKGRDLVQDLGRL 242
Db 188 EALLIQIGPKECVLPGETAGDMGKLRI--IQRGGLITERKKADFSKDIYQDLNRL 244
Qy 243 VKG-----SVEPVRLVSGFECAGALGCILSYAELADESNYNYTVKYNLSYM 294
Db 245 LKGGKGEQMSAVLPME---NQAVVSSLASAVIKFLELLSDDSNFGQFELTTDFDQYM 300
Qy 295 RLDSAAARLNVMB-SKSDANKNPSFLGLMNRCTAGMGRLLHMLKQPLLDVEENCR 353
Db 301 KLDIAAVALNLFQGSVEDITGQSQAALINK-CKTPQGQLVNVQIKQPLMDKNRIEER 359
Qy 354 LDVQSFVEDAALRODLROH-LKRISDIERLTHNLKRASLVHVVKLYQSSTVPYIKS 412
Db 360 LNLVEAFVEDAELRQTLQEDLLRRFPDLNRLAKKFORQAANLQDCYRLYQGINQLPNVIQ 419
Qy 413 VLEHDCQFATLIRERYIDSLKESDDNHLNKFGLVETSDLDQLENGEYMISSAYDPN 472
Db 420 ALEKHGKHQKLLAVFVFTPLDRLSD--FSKQEMIEITLDMQOVENHFLVPSFDPN 477
Qy 473 LSALKDQEQETLERQIHNHLKQTANDLPLDKSLDKETQFGHVFRITKKEEKKVRKQL 532
Db 478 LSELREIMNDLEKXQKQSTLISAARDLGLDPCKQIKLDSQAQFGYFRVTCKEEVLRN-- 535
Qy 533 NSHYVILETRKQGVKFTYTKLKLQDQFOKIVEYKSCQKELVARVVOATAASFSEVAGI 592
Db 536 NKNFSTVDIQKNGVKFTNSKLTSLNEEYTKNKTETEYEAQDAIVKEIWNISSGYVPMQTL 595
Qy 593 AGVLAELDVLSPADLAASCFTPTVTRNISPDPDGTGDIILEGCRHPCVEAQDWNINSINDC 652
Db 596 NDVLAQLDAVSVFAHVSNGAPVVPVRAILEKGGQRIILKASRHACVEQDEIAFINDV 655
Qy 653 RLVRGESWFOITGPNMGKSTYIRQGVNVMAOVGSFVPCDNATISIRDCIFARYGAG 712
Db 656 YFEKDKQMFHIIITGPNMGKSTYIRQGVNVMAQIGCFVPCESAESVIVDCILARVAG 715
Qy 713 DCQLRGVSTFQEMLETA SILKGTDRSLIIDLGRGTSTYDGFGLAWAICEHIVEIK 772

Db 716 DSQKGVSTFMAEMLETSATKDSLIIDELGRGTSTYDGFGLAWAISYIATKIG 775
QY 773 APTLFATHFHELTALANKNGDNHKKAGIANFHFVFAHIDPSNRKLTMLYKXVHPGACDQS 832
Db 776 AFCMPATHFHELTALAN-----QIPTVNNLHVTAL--TTEETLTMLYQVKGVCDOQS 825
QY 833 FGIHVAEFANPPSVVALAREKASELEDSPIALIPN-DIKEAASKR---KREFDRHDVS 888
Db 826 FGIHVAELANFPKXVIECAKQKALEEFQYIGESQGYDIMEPAKXCYLERE----- 878
QY 889 RGTARARQFLODFAQLPLDKMDPNVVRQKLSKXKTDL 925
Db 879 QGEKIIQEFLSKVQKMPFTEENSEENITIKLQKAEV 915
RESULT 4
US-09-651-656-3
; Sequence 3, Application US/09651656
; Patent No. 6340566
; GENERAL INFORMATION:
; APPLICANT: MCCUTHEN-MALONEY, SANDRA
; APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
; TITLE OF INVENTION: DETECTION AND QUANTITATION OF SINGLE NUCLEOTIDE
; TITLE OF INVENTION: POLYMORPHISMS, DNA SEQUENCE VARIATIONS, DNA MUTATIONS,
; TITLE OF INVENTION: DNA DAMAGE AND DNA MISMATCHES
; FILE REFERENCE: IL-10689
; CURRENT APPLICATION NUMBER: US/09/651,656
; PRIOR FILING DATE: 2000-08-29
; PRIOR FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 934
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-651-656-3
Query Match 37.9%; Score 1841.5; DB 4; Length 934;
Best Local Similarity 43.0%; Pred. No. 1.8e-164;
Matches 403; Conservative 172; Mismatches 307; Indels 55; Gaps 19;
QY 14 LKLDKQAQGFSLFFKTLKDP-RAVRLFRDRDYTSHGDDATFIAETVYHTTTALRQLG 72
Db 9 LQESAAEEVGFVRFGQMEKPTTVTLFRDGRDFTAHGEDALLAAREVFKTQGVKYM 68
QY 73 NR-ADALSSVSVRNMFETIARDILLERMDRTLELYEGSGN-----WRLVKSGETPN 124
Db 69 PAGAKNLQSVLTKMNFESFVKDLILVQYR-VEVYKRNAGKASKENDWYLAYKASPGN 127
QY 125 LGSFEDILFANNMNSPVIALAPNFGQNGCEVGLGYVDITKRVILGLTEFLDSDSHFTNL 184
Db 128 LSQFEDILFGNDMGSASIGVGVKMSAVDQGVGVYVDSIQKLGCEFFDNDQFNSL 187
QY 185 ESALVALGCRECLVP-AET-GKSEYRPMFDAISRCGVMTTERKKTPEFKGRDLVDLGR 242
Db 188 EALLIQIGKECVLPGETAGDMGLRQI--IQRGILLITERKADFTKDIYQDLNRL 244
QY 243 VKG-----SVEPRDLVSGECASGALGCLISVAELLADESNVNTVQYNLSNM 294
Db 245 LKKGKEQMNASVLPME-----NOQAVSLSLAVIKFLELLSDSNFSGQPELATTFDFSQYM 300
QY 295 RLDSAMRALNWE-SKSDANKNFSIFGLMNRCTAGMKRLLHMLKOPLDLVEINCR 353
Db 301 KLIDIAVRLNLPQGSVEDTTSQSLAALNK-CKTPQGORLVNQMIKOPLMQKRIER 359
QY 354 LDIVQSFVEDAALRQDLROH-LKRI SDIERLTHNLERKASLVHVVKLYQSSTVRYPIKS 412
Db 360 LNLVEAFVEDAELRQTLQDLLELRFEDLNLAKKFORQAQNLQDCVRLYQGINQLPNVIQ 419
QY 413 VLREHQPQATLIRERYIDSLKMSDDNHLNLPFGLVETSVDLDQLENGEMYISSAYDN 472
Db 420 ALEKHEGKQKLLAVFVTPLTDLRSD--FSKFEQMIETTLDMQDVENHEFLVKGSEFEN 477

QY 473 LSALKDEQETLERQIHNLHKQTANDLPIDKSLKDKETQGHVFRITKKEPKVRKOL 532
Db 478 LSELREIWNDEKMQSTLISAARDLGLDPGKQIKLSDSAQPGYFRVTCREEKVLRN-- 535
QY 533 NSHYIVLSTRDKGVFTYTKLKLGDQFQKIVEEYKSCQKELVARVWVQTAASFSEVFAGI 592
Db 536 KKNFSTVDIQKNGVKFTNSKLTSLNEEYTKNKTVEEBAQDAIVKEIVAINISSGVVPMQTL 595
QY 593 AGVLAELDVLLSFADLAASCTPYTRPNISPPDGTGDIILEGGRHPCVCEAOWNSIPND 652
Db 596 NDVLAQLDAVSVFAHVSNGAPVPYVRPAILEKQGRILKASHACVEVQDEIAFIPNDV 655
QY 653 RLVRGESWFQIITGNMGKSTYIRQVGVNVLMAOVGFVPCDNATISRDICIFARVGAG 712
Db 656 YFEKDKQMPHILITGNMGKSTYIRQTVIVLMAOIGCFVPCESAEVSLVDCILARVGAG 715
QY 713 DCQLRGVSTFMOEMLETSAILKATDRSLIIIDELGRGTSTYDGFGLAWAICEHIVEEIK 772
Db 716 DSQKGVSTFMAEMLETSATKDSLIIDELGRGTSTYDGFGLAWAISYIATKIG 775
QY 773 APTLFATHFHELTALANKNGDNHKKAGIANFHFVFAHIDPSNRKLTMLYKXVHPGACDQS 832
Db 776 AFCMPATHFHELTALAN-----QIPTVNNLHVTAL--TTEETLTMLYQVKGVCDOQS 825
QY 833 FGIHVAEFANPPSVVALAREKASELEDSPIALIPN-DIKEAASKR---KREFDRHDVS 888
Db 826 FGIHVAELANFPKXVIECAKQKALEEFQYIGESQGYDIMEPAKXCYLERE----- 878
QY 889 RGTARARQFLODFAQLPLDKMDPNVVRQKLSKXKTDL 925
Db 879 QGEKIIQEFLSKVQKMPFTEENSEENITIKLQKAEV 915

RESULT 5

US-09-650-855-3
; Sequence 3, Application US/09650855
; Patent No. 6365355
; GENERAL INFORMATION:
; APPLICANT: MCCUTHEN-MALONEY, SANDRA
; APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
; TITLE OF INVENTION: CHIMERIC PROTEINS FOR DETECTION AND QUANTITATION OF DNA
; TITLE OF INVENTION: MUTATIONS, DNA SEQUENCE VARIATIONS, DNA DAMAGE AND DNA
; TITLE OF INVENTION: MISMATCHES
; FILE REFERENCE: IL-10284
; CURRENT APPLICATION NUMBER: US/09/650,855
; CURRENT FILING DATE: 2000-08-29
; PRIOR FILING DATE: 60/192,764
; PRIOR FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 934
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-650-855-3

Query Match 37.9%; Score 1841.5; DB 4; Length 934;
Best Local Similarity 43.0%; Pred. No. 1.8e-164;
Matches 403; Conservative 172; Mismatches 307; Indels 55; Gaps 19;
QY 14 LKLDKQAQGFSLFFKTLKDP-RAVRLFRDRDYTSHGDDATFIAETVYHTTTALRQLG 72
Db 9 LQESAAEEVGFVRFGQMEKPTTVTLFRDGRDFTAHGEDALLAAREVFKTQGVKYM 68
QY 73 NR-ADALSSVSVRNMFETIARDILLERMDRTLELYEGSGN-----WRLVKSGETPN 124
Db 69 PAGAKNLQSVLTKMNFESFVKDLILVQYR-VEVYKRNAGKASKENDWYLAYKASPGN 127
QY 125 LGSFEDILFANNMNSPVIALAPNFGQNGCEVGLGYVDITKRVILGLTEFLDSDSHFTNL 184
Db 128 LSQFEDILFGNDMGSASIGVGVKMSAVDQGVGVYVDSIQKLGCEFFDNDQFNSL 187

185 ESALVALGCRECLVP-AET-GKSSEYRPMFDAISRCGVMMVTERKKTBFKGRDLVDQLGRL 242
186 EALLIQIGPKCEVLPGGETAGDMGKLRIQI---IQRGGLLITERKADFSKDIYQDLNRL 244
243 VKG-----SVEPVDLVSGFECASGALGCIILSYAELLADESNYNYTVKQYNLSYM 294
245 LKGGKQGMNSAVLPME---NQAVSSLSAVIKFLELLSDSNFQGFELTTDFDSQYM 300
295 RLDSAAARALNVMB-SKSDANKNFSLFLMNRCTTAGMKRLHMLKQPLLDVEEINCR 353
301 KLDIAAVALNLPFGSVEDTTGSQSLAALNK-CKTQGOQLVNVQWIKQPLMDKRNREER 359
354 LDLVQSVFEDAALQDLRQH-LKRSIDIERLTHNLKRASLVHVVKLYQSTSRVPYIKS 412
360 LNLVEAFVEDAEALRQTLQEDLLRRFPDLNRLAKKFORQAANLQDCYRLQINGQLPNVIQ 419
413 VLEHDSQFATLIBERYIDSLKESDDNHLNKFGLVETSDLDLENGEYMWISADPN 472
420 ALEKHGKHQKLLAVFVPLTDLRSD--FSKQFEMIETLDMQVENHEFLVPSFDPN 477
473 LSALKDQEQETLEROIHNHKTANDLDPIDKSLDKETOFGHVFRITTKKEEPPKVRKQL 532
478 LSELREIMNDLEKXQKQSLISAARDLGLDPCKQIKLDSSAQFGYFVFTCKEVLN-- 535
533 NSHVIVLETRKDGKVFYTKLKLGDQFQKIVERYKSCQKELVARVQTAASFSEVFAGI 592
536 NKNFSTVDIQKGVKFTNSKLTSLNEEYTKNTEVEEAQDAIVKEIVNISGYSVEPMQTL 595
593 AGVLAEIDLVSFADLAASCTPYTRPNI SPDPDGDIIILEGCRHPCVCEADWNSIPNDC 652
596 NDVLAQDLDAVVSFAHVSNGAPVYVPRPAILEKQGRILKASRHACVEVQDEIAFIPNDV 655
653 RLVRGESWFOIITGPNMGKSTYIRQGVNVLMQVGSFVPCDNATISIRDCIFARVGAG 712
656 YFEKDKQMFHIIITGPNMGKSTYIRQGVNVLMQVGSFVCEASNEVSIVDCILARVGAG 715
713 DCQLRGVSTFQEMLETAIILKQATDRSLIIDIELGRGTSTYDGFGLAWAICEHIVEIK 772
716 DSQKGVSTFMAEMLETAIILRSATKDSLIIDIELGRGTSTYDGFGLAWAISEVIATKIG 775
773 APTLFATHFELTALANKGNGHKKNAGIANFVFAHIDPSNRKLTMLYKVVHFGACDQS 832
776 AFCMFATHFELTALAN-----QIPTVNNLHVTL--TTEETLTMLYQVKKGVCDQS 825
833 FGIHVAEPANPPPSVVALAREKASELEDFSPALIPN-DIKEAASKR---KREFDRHDVS 888
826 FGIHVAELANFPKHVIECAKQKALEEFQYIGESQGYDIMEPAKKCYLERE----- 878
889 RGTARARQLODFAQLPDLKMDPNVVRQKLSKMTDL 925
879 QGEKIIQEFLSKVQKMPFTEENSEENITIKLQKAEV 915

RESULT 6

US-09-708-200-13
; Sequence 13, Application US/09708200
; Patent No. 6576468
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas C
; APPLICANT: Grasso, Luigi
; APPLICANT: Sags, Philip M
; TITLE OF INVENTION: METHODS FOR ISOLATING NOVEL ANTIMICROBIAL AGENTS FROM
; TITLE OF INVENTION: HYPERMUTABLE CELLS
; FILE REFERENCE: MOR-0005
; CURRENT APPLICATION NUMBER: US/09/708,200
; CURRENT FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 934
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-708-200-13

Query Match 37.9%; Score 1841.5; DB 4; Length 934;
Best Local Similarity 43.0%; Pred. No. 1.8e-164;
Matches 403; Conservative 172; Mismatches 307; Indels 55; Gaps 19;

QY 14 LKLDKAOQAOQFLSFFKTLPKDP-RAVELFDRDRDYVYTHGDDATFIATYHTTTALRQLG 72
DB 9 LQLEAAAEVGFVRFFQGMPEKPTTVALDFRDGDPYTAHGEDALLAAREVFVKTGKVMG 68
QY 73 NR-ADALSSYSVSRNMEETIARDILLERMORTLELYEGSGSN-----WELVKSQTPGN 124
DB 69 PAGAKNLQSVVLSKQNFESFVKDILLVRYQR-VBYVKNRAGNKASKENDWYLAJKASPN 127
QY 125 LGSFEDILFANNEMQNSPVTAALAPNFGQNGCEVGLGVYDITKRVGLGITEFLDDSHFNL 184
DB 128 LSQFEDILFGNNDMSASIGVVGVKMSAVDQORQGVGVDSIQKGLGCEFPDNDQSNL 187
QY 185 ESALVALGCRECLVP-AET-GKSSEYRPMFDAISRCGVMMVTERKKTBFKGRDLVDQLGRL 242
DB 188 EALLIQIGPKCEVLPGGETAGDMGKLRIQI---IQRGGLLITERKADFSKDIYQDLNRL 244
QY 243 VKG-----SVEPVDLVSGFECASGALGCIILSYAELLADESNYNYTVKQYNLSYM 294
DB 245 LKGGKQGMNSAVLPME---NQAVSSLSAVIKFLELLSDSNFQGFELTTDFDSQYM 300
QY 295 RLDSAAARALNVMB-SKSDANKNFSLFLMNRCTTAGMKRLHMLKQPLLDVEEINCR 353
DB 301 KLDIAAVALNLPFGSVEDTTGSQSLAALNK-CKTQGOQLVNVQWIKQPLMDKRNREER 359
QY 354 LDLVQSVFEDAALQDLRQH-LKRSIDIERLTHNLKRASLVHVVKLYQSTSRVPYIKS 412
DB 360 LNLVEAFVEDAEALRQTLQEDLLRRFPDLNRLAKKFORQAANLQDCYRLQINGQLPNVIQ 419
QY 413 VLEHDSQFATLIBERYIDSLKESDDNHLNKFGLVETSDLDLENGEYMWISADPN 472
DB 420 ALEKHGKHQKLLAVFVPLTDLRSD--FSKQFEMIETLDMQVENHEFLVPSFDPN 477
QY 473 LSALKDQEQETLEROIHNHKTANDLDPIDKSLDKETOFGHVFRITTKKEEPPKVRKQL 532
DB 478 LSELREIMNDLEKXQKQSLISAARDLGLDPCKQIKLDSSAQFGYFVFTCKEVLN-- 535
QY 533 NSHVIVLETRKDGKVFYTKLKLGDQFQKIVERYKSCQKELVARVQTAASFSEVFAGI 592
DB 536 NKNFSTVDIQKGVKFTNSKLTSLNEEYTKNTEVEEAQDAIVKEIVNISGYSVEPMQTL 595
QY 593 AGVLAEIDLVSFADLAASCTPYTRPNI SPDPDGDIIILEGCRHPCVCEADWNSIPNDC 652
DB 596 NDVLAQDLDAVVSFAHVSNGAPVYVPRPAILEKQGRILKASRHACVEVQDEIAFIPNDV 655
QY 653 RLVRGESWFOIITGPNMGKSTYIRQGVNVLMQVGSFVPCDNATISIRDCIFARVGAG 712
DB 656 YFEKDKQMFHIIITGPNMGKSTYIRQGVNVLMQVGSFVCEASNEVSIVDCILARVGAG 715
QY 713 DCQLRGVSTFQEMLETAIILKQATDRSLIIDIELGRGTSTYDGFGLAWAICEHIVEIK 772
DB 716 DSQKGVSTFMAEMLETAIILRSATKDSLIIDIELGRGTSTYDGFGLAWAISEVIATKIG 775
QY 773 APTLFATHFELTALANKGNGHKKNAGIANFVFAHIDPSNRKLTMLYKVVHFGACDQS 832
DB 776 AFCMFATHFELTALAN-----QIPTVNNLHVTL--TTEETLTMLYQVKKGVCDQS 825
QY 833 FGIHVAEPANPPPSVVALAREKASELEDFSPALIPN-DIKEAASKR---KREFDRHDVS 888
DB 826 FGIHVAELANFPKHVIECAKQKALEEFQYIGESQGYDIMEPAKKCYLERE----- 878
QY 889 RGTARARQLODFAQLPDLKMDPNVVRQKLSKMTDL 925
DB 879 QGEKIIQEFLSKVQKMPFTEENSEENITIKLQKAEV 915

RESULT 7

US-09-788-657-19
; Sequence 19, Application US/09788657

Patent No. 6656736
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas
; APPLICANT: Sasa, Philip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Grasso, Luigi
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Methods for generating hypermutable
; TITLE OF INVENTION: yeast
; FILE REFERENCE: 01107.00097
; CURRENT APPLICATION NUMBER: US/09/788,657
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,336
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 934
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-657-19

Query Match 37.9%; Score 1841.5; DB 4; Length 934;
Best Local Similarity 43.0%; Pred. No. 1.8e-164;
Matches 403; Conservative 172; Mismatches 307; Indels 55; Gaps 19;

QY 14 LKLDKQAGGFLSFEKTLPKDP-RAVRLFDREDDYVTSCHDDATFTAEVYHTTALROLG 72
DB 9 LQESAAEEVGFVRFQGMPEKPTTVRLFDGRDFTAHGEDALLAAREVFKTQGVKYM 68

QY 73 NR-ADALSSVSVRNMFTIARDILLERMDRTLEYEGSGN-----WRLVKSSTP 124
DB 69 PAGAKNLQSVLVSKMNFESFVKDLLLVQYR-VEVYKNRAGNKASKENDWYLAYKSPGN 127

QY 125 LGSFEDILPANNEMQNSPVIALAPNFQNGCEVGLGVVDITKRVLGLTEFLDDSHFTNL 184
DB 128 LSQFEDILLGNNDMSASIGVGVKMSAVDQQRQGVGVYVDSIQRLKGLCEFPDQFNSL 187

QY 185 ESALVALGCRECLVP-AET-GKSSEYRPMFDAISRCGVVMVTERKTEKFGRLVDLGR 242
DB 188 EALLIQIGKECVLPGETAGDMKLRQI---IQGGILITERKADSTKDIYQDLNRL 244

QY 243 VKG-----SVEPVRDLVSGFECASGALGCIISYAEILLADESNYGVYVQYMLNSYM 294
DB 245 LKGGKEQMSAVLPME-----NOVAVSSLSAVIRKLELLSDSNFGQPELTTFDSQYM 300

QY 295 RLDSAMRALNME-SKSDANKNFSFLGLMNTCTAGMKRLLHMLKOPLLDVEEINCR 353
DB 301 KLDIAAVALNLFQGSVEDTTGSSLAALLNK-CKTPQGRVLVQWIKQPLMDKNRIER 359

QY 354 LDVOSFVEDAALRODLROH-LKRISDIERTLTHNLERKASLVHVVKLQSSSTRVPIKS 412
DB 360 LNLVEAFVEDAELRLQEDLLRRFPDNLRAKKFORQANLQDCVRLYQGINQIPNVIQ 419

QY 413 VLHDGQFATLIRERYIDSLSEKNSDDNHLNFKIGLVETSVLDQLENGEYMISSAYDN 472
DB 420 ALEKHBGKHQLLAVFVTPPLDLRSD--FSKQEMIEITLDMQDVENHEFLVKPSFDN 477

QY 473 LSALKDQETLRLERQINHLKQFANDLDPIDKSLKLDKETQGHVPRITKPEKPKVKQL 532
DB 478 LSELREIMNDLEKMQOSTLISAARDLGLDPGKQLKLDSSAQFGYVPRVTCKEKVLN-- 535

QY 533 NSHYIVLETRKQGVKFTYTKLKGQFOKI VEEYKSCOKELVARVQTAASFSEVFAGI 592
DB 536 KNKFSVTDIQKGVKFTNSKLSNEEYTKNTEYEEAQDAIWEIUNISSGVPEMQIL 595

QY 593 AGVLAELVLLSPADLAASCPTPYTPNISPDTGDIILEGCRHPCVEAQDWNSIPNDC 652
DB 596 NDVLAQLDAVVSFAHVSNGAPVYVVRPAILEKQGRILLKSEHACVVEQDEIAFIPNDV 655

QY 653 RLVRGSEWFTQITGPNMGKSTYIROGVNVLMAQVGSFVPCDNATISTDCIFARVGAG 712
DB 656 YFEKQMFHITGPNMGKSTYIROTGVIVLMAQICGFCVPCESAEVSVDCILARVGAG 715

QY 713 DCOLRGVSTFMOEMLETASILKGGATDRSLIITIDELGRGTSTYDGFGLAWAICEHIVERIK 772
DB 716 DSQKGVSTFNAEMLETASILRSATKOSLIITIDELGRGTSTYDGFGLAWAISEYATYKIG 775

QY 773 APTLFATHFHELTALANKNGDNGHKQAGIANFHVFAHIDPSNRKLTWLYKVHPGACDOS 832
DB 776 AFCMFATHFHELTALAN-----QIPTVNNLHVTA--TTEETLTWLYQVKGVCQDOS 825

QY 833 FGIHVAEPANPPSVVALAREKASELEDSPSIALIPN-DIKEAASKR---KREPDHDSV 888
DB 826 FGIHVAELANFPKHVIECAKOKALEEFEFQVIGSSQGYDIMEPAKCKYLERE----- 878

QY 889 RGTARARQFLQDFAQLPLDKMDPNVRQKLSKMKTDL 925
DB 879 QGEKLIQFSLKVKQMPTEENSEENIITIKLQKLAEV 915

RESULT 8
US-09-512-250C-31
; Sequence 31, Application US/09512250C
; Patent No. 6518042
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben
; APPLICANT: Petersen, [Executor for Lars Christiansen, deceased], Dennis
; APPLICANT: Vind, Jesper
; TITLE OF INVENTION: A process for Making DNA Libraries In Filamentous Fungal Cells
; TITLE OF INVENTION: No. 6518042el Cloned Gene Involved in the Mismatched Repair Syst
; TITLE OF INVENTION: Cells
; FILE REFERENCE: 5718.200-US
; CURRENT APPLICATION NUMBER: US/09/512,250C
; CURRENT FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 1010
; TYPE: PRT
; ORGANISM: human.p
US-09-512-250C-31

Query Match 37.9%; Score 1841.5; DB 4; Length 1010;
Best Local Similarity 43.0%; Pred. No. 2.1e-164;
Matches 403; Conservative 172; Mismatches 307; Indels 55; Gaps 19;

QY 14 LKLDKQAGGFLSFEKTLPKDP-RAVRLFDREDDYVTSCHDDATFTAEVYHTTALROLG 72
DB 85 LQESAAEEVGFVRFQGMPEKPTTVRLFDGRDFTAHGEDALLAAREVFKTQGVKYM 144

QY 73 NR-ADALSSVSVRNMFTIARDILLERMDRTLEYEGSGN-----WRLVKSSTP 124
DB 145 PAGAKNLQSVLVSKMNFESFVKDLLLVQYR-VEVYKNRAGNKASKENDWYLAYKSPGN 203

QY 125 LGSFEDILPANNEMQNSPVIALAPNFQNGCEVGLGVVDITKRVLGLTEFLDDSHFTNL 184
DB 204 LSQFEDILLGNNDMSASIGVGVKMSAVDQQRQGVGVYVDSIQRLKGLCEFPDQFNSL 263

QY 185 ESALVALGCRECLVP-AET-GKSSEYRPMFDAISRCGVVMVTERKTEKFGRLVDLGR 242
DB 284 EALLIQIGKECVLPGETAGDMKLRQI---IQGGILITERKADSTKDIYQDLNRL 320

QY 243 VKG-----SVEPVRDLVSGFECASGALGCIISYAEILLADESNYGVYVQYMLNSYM 294
DB 321 LKGGKEQMSAVLPME-----NOVAVSSLSAVIRKLELLSDSNFGQPELTTFDSQYM 376

QY 295 RLDSAMRALNME-SKSDANKNFSFLGLMNTCTAGMKRLLHMLKOPLLDVEEINCR 353
DB 377 KLDIAAVALNLFQGSVEDTTGSSLAALLNK-CKTPQGRVLVQWIKQPLMDKNRIER 435

QY 354 LDVOSFVEDAALRODLROH-LKRISDIERTLTHNLERKASLVHVVKLQSSSTRVPIKS 412
DB 436 LNLVEAFVEDAELRLQEDLLRRFPDNLRAKKFORQANLQDCVRLYQGINQIPNVIQ 495

QY 413 VLHDGQFATLIRERYIDSLSEKNSDDNHLNFKIGLVETSVLDQLENGEYMISSAYDN 472

Db 496 ALEHGEHQKLLAVFVPLTLDRSD--FSKFOEMIETTLDMQVENHEELVKPSFDPN 553
Qy 473 LSALKDEQETLEROIHLNHLKQTANDLDPIDSKLDKETOFQGHVFRITTKKEEPKVRKQL 532
Db 554 LSELEINMDLEKXMQSLISAARDLGLDPQKQIKLSDSAGFYFRVTCKEEKVLNR-- 611
Qy 533 NSHYVILETRKDGKFTYTKLKLGDQPKQKIVEEYKSCQKELVARVQTAASFSEVFAGI 592
Db 612 KNFSTVDIQKNGVKFTNSLTSLNEEYTKNTEVEEAQDAIVKEIVNISGGYVEPMQTL 671
Qy 593 AGVLAELDVLLSPADLAASCTPYTRPNISPPDGDIIILEGRHPCVBAQDWNVNSIPND 652
Db 672 NDVLAQLDAVVSFAHVSNGAPVYVRPAILEKQGRRIILKASHACVEVQDEIAFIPNDV 731
Qy 653 RLVRGESWFQIITGNMGKSTYIRQGVNVLMAQVGSFVPCDNATISIRDCIFARVGAG 712
Db 732 YFEKDKQFHIITGNMGKSTYIRQGVNVLMAQVGSFVPCDNATISIRDCIFARVGAG 791
Qy 713 DCQLRGVSTFMOEMLTASILKLGATDRSLIIIDELGRGTSTYDGFGLAWAICEHIVEIK 772
Db 792 DSQKGVSTFMAEMLTASILRSATKOSLIIIDELGRGTSTYDGFGLAWAISEYIATKIG 851
Qy 773 APTLFATHFHELTALANKNGDHKKNGAGIANFVFAHIDPSNRKLTMLYKVHPGACDQS 832
Db 852 AFCMFATHFHELTALAN-----QIPTVNNLHVTL--TTEETLTMLYQVKKGVCDQS 901
Qy 833 FGIHVAEFANPPSVVALAREKASELEDFSPAIIPN-DIKEAASKR---KREFDRHDVS 888
Db 902 FGIHVAELANPKHIVIECAKQKALELEEFQVIGESQGVDMPEAKKCYLBER----- 954
Qy 889 RGTARAKFLQDFAQLPLDKMDPNVVRKLSKMTDL 925
Db 955 QGEKIIQFSLKVKQMPTEENSEENITIKLQKLAEV 991

RESULT 9

US-09-512-250C-33
; Sequence 33, Application US/09512250C
; Patent No. 6518042
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben
; APPLICANT: Pedersen (Executor for Lars Christiansen, deceased), Dennis
; APPLICANT: Vind, Jesper
; TITLE OF INVENTION: A process for Making DNA Libraries in Filamentous Fungal Cells
; TITLE OF INVENTION: No. 6518042el Cloned Gene Involved in the Mismatched Repair Sys
; FILE REFERENCE: 5718.200-US
; CURRENT APPLICATION NUMBER: US/09/512,250C
; CURRENT FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 935
; TYPE: PRT
; ORGANISM: mus. p.
US-09-512-250C-33

Query Match 37.4%; Score 1818.5; DB 4; Length 935;
Best Local Similarity 42.3%; Pred. No. 2.7e-162;
Matches 395; Conservative 173; Mismatches 318; Indels 47; Gaps 18;

Qy 14 LKLDKAKOQGFSLFPTLPKDP-RAVRLFRDRDYVTSHGDDATFIAETVYHTTALRLG 72
Db 9 LQLEGAAGVRFEGNPEKSTVRLFRDGDFTANGEDALLAAREVFTQGVKYM 68
Qy 73 NR-ADAGSSVSVRNMFTIARDILLERMDRTLEYEGSGN-----WELVKSGTGPN 124
Db 69 PAGSKTLQSVLSKMFESFVKDLLLVQRX-VEVYKKNAGKASKAKENWYLAFAKSPGN 127
Qy 125 LGSFEDILFANNQNSVIAALAPNFQNCCEVLGVYDITKRVLGLTEFLDSSHNTNL 184
Db 128 LQSFEDILFGNNDNSASVGVNGIKMAVVDGQRHVGVYDSTQRKGLCEPPENDQFSNL 187

Qy 185 ESALVALGCRECLVPA--ETGKSSEYRPMFDAISRCQGMVMTERTKTEPKGRDLVDQLGRL 242
Db 188 EALLIQIGPKECVLPGGETTGDGKLR---QVIRGGILLITERRADSTKDIQDINRL 244
Qy 243 VKGSV-BPVRDLV---SGFECASGALGCIISYABELLADENSYNYTVYKQNLNLSYMRIDS 298
Db 245 LKGGKGEQINSAALPEMENQVAVSSLSAVIKFLELLSDSNFGQFELATFDSQMKLDM 304
Qy 299 AAMPALNME-SKSDANKNPSLFGIMNRTCTAGCKRLLHMLKQPLLDVSEINCRDLV 357
Db 305 AAVRALNLFQGSVEDTTGQSQAALANK-KCTAQOQRLVNMQIKPLMDRNIERLNLV 363
Qy 358 QSFVEDAALRODLROH-LKRISDIERTLNLERRKASLVHVVKLYQSSTRVPYKSVLER 416
Db 364 EAFVEDSELRSQLOEDLLRRPDLNRLAKRFQOAAANLQDCYRLYOGINQPLPSVQALEK 423
Qy 417 HDGQFATLIIRERYTDSLEKMSDDNHLANKFGLVTSVDLDQLENGEYMISSAYDPNLSAL 476
Db 424 YEGRHQALLAVFVPLTIDLRSD--FSKFOEMIETTLDMQVENHEFLVKPSFDPNSEL 481
Qy 477 KDEQETLEROIHLNHLKQTANDLDPIDSKLDKETOFQGHVFRITTKKEEPKVRKQLNSHY 536
Db 482 REVMDGLEKXMQSLINAARGLDGDPKQIKLSDSAGFYFRVTCKEEKVLNR--KNKF 539
Qy 537 IVLETRKDGKFTYTKLKLGDQPKQKIVEEYKSCQKELVARVQTAASFSEVFAGIAGVL 596
Db 540 STVDIQKNGVKFTNSLSENEEYTKNKEVEEAQDAIVKEIVNISGGYVEPMQTLNDVL 599
Qy 597 AELDVLLSPADLAASCTPYTRPNISPPDGDIIILEGRHPCVBAQDWNVNSIPNDCLVR 656
Db 600 AHLDAIVSFAHVSNAAPVYVRPAILEKQGRRIILKASHACVEVQDEVAFIPNDVHPEK 659
Qy 657 GESWFQIITGNMGKSTYIRQGVNVLMAQVGSFVPCDNATISIRDCIFARVGACDQL 716
Db 660 DKQMFHIITGNMGKSTYIRQGVNVLMAQVGSFVPCDNATISIRDCIFARVGACDQL 719
Qy 717 RGVSTFMOEMLTASILKLGATDRSLIIIDELGRGTSTYDGFGLAWAICEHIVEIKAPTL 776
Db 720 KGVSTFMAEMLTASILRSATKOSLIIIDELGRGTSTYDGFGLAWAISDYATKIGAFCM 779
Qy 777 FATHFHELTALANKNGDHKKNGAGIANFVFAHIDPSNRKLTMLYKVHPGACDQSGFIH 836
Db 780 FATHFHELTALAN-----QIPTVNNLHVTL--TTEETLTMLYQVKKGVCDQSFGIH 829
Qy 837 VAEFANPPSVVALAREKASELEDFSPAIIPNDIKEAASKR---REFDRHDVSRGTA 892
Db 830 VAELANFPRHVIAKQKALELEEFQVIGTSLGCDCEAPPAKRCCLERE-----QGEK 882
Qy 893 RARQFLQDFAQLPLDKMDPNVVRKLSKMTDL 925
Db 883 IILEFLSKVKQVPTAMSESSISAKLQKLAEV 915

RESULT 10

US-09-512-250C-2
; Sequence 2, Application US/09512250C
; Patent No. 6518042
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben
; APPLICANT: Pedersen (Executor for Lars Christiansen, deceased), Dennis
; APPLICANT: Vind, Jesper
; TITLE OF INVENTION: A process for Making DNA Libraries in Filamentous Fungal Cells
; TITLE OF INVENTION: No. 6518042el Cloned Gene Involved in the Mismatched Repair Sys
; FILE REFERENCE: 5718.200-US
; CURRENT APPLICATION NUMBER: US/09/512,250C
; CURRENT FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 940
; TYPE: PRT

QY	35	PAVRLEFDRDDYYTSHGDDATFIA-----ETYHTTTALTALQGNRADALSSVSR	85
Db	36	PDYLLLFQVGDFYECFGEDAERLARGLVLTHTKSODFTTPMAGIPARA-----	85
QY	86	NWPFETIARDII-----LERMDRTLELYEGSGSNWR-LVKSCTPGNIGSPEDILFANNMQ	139
Db	86	----FDYAEERLLKMGFRILAVADQVEPAEAEGLVRREVTOQLLTGPTL--TOEALL	137
QY	140	NSPVIUALAPNFGQNGCEVLGYVDIFK-----RVLGLTEFLDDSHFTNLESALVALGCR	194
Db	138	EANYLAIAATGDGW-----GLAFIDVSTGEFKGTLTKSKSALYDELFRR-----	182
QY	195	ECLVPAFTGKSSEYRPMFDALSRGVMVTRKKTEFKGRDLVODLGRLVKGSVPVRDLV	254
Db	183	----PAKVLLIAPELRE-----NEAFVAEFRKRPVW-----LSEAPFEPQGEPR	222
QY	255	SGFECASGALCIIISYAELLADESNYNTYVKQYNL---NSYMRLDSAAAMRALNVMESKS	311
Db	223	LALRRQAQAL---LAYAR-----ATQGGALSVRFRLYDPGAFVRLPEALSLEAVEPELR	275
QY	312	DANKNFSLFGLMNRCTAGMGKRLHLHMLKQPLDVBEEINCRLLDLVQSFVEDAALRQDLR	371
Db	276	QGD---TLFGVLDETRTA-PGRLLLOALWLRHPLERGPLEARLDLVRVFRSGALAREGV	331
QY	372	OHLKRISDIERLTNHLERKASLVHVVKLYQSSTRVPYIKSVLERHDGOFATLIRERYD	431
Db	332	RLLFRLADLERLATRLELSRASPRDLAALRRSLIIPELKGL-----ENGEYMISSAYDNLSALKD	478
QY	432	SLEKWSDDNHLNKTIGLVETSVOLDQJ-----LGESEVGPDLSGLLEELRAALVEDPPLKVS	478
Db	374	-----LGESEVGPDLSGLLEELRAALVEDPPLKVSSEGG--LIRRGYDPPDLDAURR	421
QY	479	EOETTLERQIHLNKHQTANDLPLDKSLKLDKETQFGHVFRITKKBEPKVRQLNSHYIV	538
Db	422	AHAEGVAYFLDEAREKERTGP--TLKGVNAVFGYILEVTRPYVEKVPQE---XRP	474
QY	539	LETBKDGWKVFTYKLKLGDOFQKIVBEYKSCQELVARVVOVTAASFSVEFAGIAGVLAE	598
Db	475	VQTLKDRQRYTLPEMKERERELYLEALIKRRESEVFALARREARKEAEALREAAARILAE	534
QY	599	LDVLISFADLAASCPPTPVTRNISPDPDGTDLLEGCBHPQCEAQDWNSTFNDCLVRGE	658
Db	535	LDVYAALAEAVR--HGVRTFRFGE---RLRIRAGRHVPVVER--TAFVNDPLEWAHE-	585
QY	659	SWFOITIGPNMGKSTYIRQVGVNVLMAQVGSFVPCDNATISIRDCIFARVGAGDQCLRG	718
Db	586	--LVLVTGPNMAGKSTFLRQTALALLAQIGSFVPAEAEELPFDGIIYTRIGASDDLAGG	643
QY	719	VSTFMQEMLETAIIUKGATDSRLSIIIDELRGSTSYDYGFLGNAWACHHIVEETKATFLA	778
Db	644	KSTFVMEVEEVALVLKEATERSVLDDVEGRGTSGLDGVATATALAE-ALHERRCYTLFA	702
QY	779	THFHEITALANKNGDNHKKNAGTANFHVFAHIDPSNRKLTMLYKHPGACDQSGFHVA	838
Db	703	THYFELTALALPR-----LKNLHVAKEEKG--LVFHVQVLPGPASKSYGTEVA	750
QY	839	EFANFPSPSYVALAREKASEL	858
Db	751	EWAGLPKFYVTRARAILSAM	770

RESULT 14

RESOL 14
US-09-650-855-15
; Sequence 15, Application US/09650855
; Patent No. 6365355
; GENERAL INFORMATION:
; APPLICANT: MCGUTHEN-MALONEY, SANDRA
; APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
; TITLE OF INVENTION: CHIMERIC PROTEINS FOR DETECTION AND QUANTIFICATION OF DNA
; TITLE OF INVENTION: MUTATIONS, DNA SEQUENCE VARIATIONS, DNA DAMAGE AND DNA
; TITLE OF INVENTION: MISMATCHES
; FILE REFERENCE: IL-10284

Db 751 EMAGLPKEVVVERARALISAM 770

RESULT 15

US-09-651-656-1
 ; Sequence 1, Application US/09651656
 ; Patent No. 6340566
 ; GENERAL INFORMATION:
 ; APPLICANT: MCCUTHEN-MALONEY, SANDRA
 ; APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
 ; TITLE OF INVENTION: DETECTION AND QUANTITATION OF SINGLE NUCLEOTIDE
 ; TITLE OF INVENTION: POLYMORPHISMS, DNA SEQUENCE VARIATIONS, DNA MUTATIONS,
 ; TITLE OF INVENTION: DNA DAMAGE AND DNA MISMATCHES
 ; FILE REFERENCE: IL-10689
 ; CURRENT APPLICATION NUMBER: US/09/651,656
 ; CURRENT FILING DATE: 2000-08-29
 ; PRIOR APPLICATION NUMBER: 60/192,764
 ; PRIOR FILING DATE: 2000-03-28
 ; NUMBER OF SEQ ID NOS: 106
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 240
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-651-656-1

Query Match 14.9%; Score 724.5; DB 4; Length 240;
 Best Local Similarity 62.4%; Pred. No. 6e-60;
 Matches 153; Conservative 22; Mismatches 59; Indels 11; Gaps 3;
 Qy 635 RHPCEAQQDWNSIPNDCRLVRGESWFIITGPNMGKSTYIRQVGVNVLMAQVGSFVPC 694
 Db 2 RHACVEQDEIAFIPNDVYFEKQKMFHIIITGPNMGKSTYIRQVGVNVLMAQVGSFVPC 61
 Qy 695 DNATISIRDCIFARVAGAGDQCLRGVSTFPMOEMLETSILKGAIDRSIIIIIDELGRGTSTY 754
 Db 62 ESAEVSIVDCILARVAGAGDQCLRGVSTFPMOEMLETSILKGAIDRSIIIIIDELGRGTSTY 121
 Qy 755 DGFGLAWAICEHIVEEIKAPTLPATHEHETALANKNGDNHKKNGKAGIANFHYFAHIDPS 814
 Db 122 DGFGLAWAISEYATKIGAFCMFATHFHELTALAN-----QIPTVNNLHVLTAL--TT 171
 Qy 815 NRKLTMLYKVPAGACDOSFGIHVAEPANFPSPVVALAREKASELEDFSPAIIPN-DIKE 873
 Db 172 EETLTMLYQVKKGVCDQSFQIHVAELANFPKHVIECAKQKALELEEFQYICESQGYDIME 231
 Qy 874 AASKR 878
 Db 232 PAAKK 236

Search completed: April 7, 2004, 10:47:31
 Job time : 27 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 7, 2004, 10:46:01 ; Search time 53 Seconds
(without alignments)
4653.070 Million cell updates/sec

Title: US-10-029-065-2
Perfect score: 4859
Sequence: 1 MNENLEQSKLPELKLDAKO.....KMKTDLERDAVSHWLQOFF 939

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1071772 seqs, 262633353 residues

Total number of hits satisfying chosen parameters: 1071772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	4859	100.0	939	14	US-10-029-065-2
2	4856	99.9	937	14	US-10-029-065-4
3	3629	74.7	937	14	US-10-270-839-49
4	3082.5	63.4	860	12	US-10-425-114-56470
5	2358	48.5	592	12	US-10-424-599-214104
6	2004.5	41.3	567	12	US-10-424-599-214104
7	1842.5	37.9	934	14	US-10-109-791A-66
8	1841.5	37.9	934	9	US-09-788-657-19
9	1841.5	37.9	934	10	US-09-912-697-10
10	1841.5	37.9	934	10	US-09-760-285-20
11	1841.5	37.9	934	14	US-10-270-839-31
12	1841.5	37.9	934	14	US-10-243-130-11
13	1841.5	37.9	934	14	US-10-371-857-5
14	1841.5	37.9	934	14	US-10-371-634-9
15	1841.5	37.9	934	14	US-10-348-074-7

SUMMARIES

ALIGNMENTS

RESULT 1

US-10-029-065-2
; Sequence 2, Application US/10029065
; Publication No. US20030150024A1
; GENERAL INFORMATION:
; APPLICANT: May, Gregory
; APPLICANT: Baszczyński, Christopher
; APPLICANT: Zhu, Tong
; APPLICANT: Kipp, Peter
; APPLICANT: Mahajan, Pramod
; TITLE OF INVENTION: PLANT MSH2 SEQUENCES AND METHODS OF USE
; FILE REFERENCE: 5839-2 (035839/196219)
; CURRENT APPLICATION NUMBER: US/10/029,065
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENG-H: 939
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-10-029-065-2

Query Match 100.0%; Score 4859; DB 14; Length 939;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 939; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNENLEQSKLPELKLDAKOQGFSLPKDPRAVRLPDRDYTSHGDDATFTAAET 60
Db 1 MNENLEQSKLPELKLDAKOQGFSLPKDPRAVRLPDRDYTSHGDDATFTAAET 60

QY 61 YYHTTTALRQLGNRADALSSVSRNMFETIARDILLERMDRTILEYEGSGSNRLVKSG 120
Db 61 YYHTTTALRQLGNRADALSSVSRNMFETIARDILLERMDRTILEYEGSGSNRLVKSG 120

QY 121 TPGNLGSPEDILFANNEMQNSPVIAALAPNGQGVGLGYVDITKRVGLTFLDSSH 180
Db 121 TPGNLGSPEDILFANNEMQNSPVIAALAPNGQGVGLGYVDITKRVGLTFLDSSH 180

Sequence 13, Appl
Sequence 277, App
Sequence 4282, A
Sequence 3873, Ap
Sequence 129, App
Sequence 2022, Ap
Sequence 37, Appl
Sequence 65, Appl
Sequence 125, App
Sequence 172, App
Sequence 124, App
Sequence 284633,
Sequence 4999, Ap
Sequence 11322, A
Sequence 12632, A
Sequence 9740, Ap
Sequence 74805, A
Sequence 19983, A
Sequence 12333, A
Sequence 5274, Ap
Sequence 44374, A
Sequence 70970, A
Sequence 11784, A
Sequence 72450, A
Sequence 51818, A
Sequence 52510, A
Sequence 53164, A
Sequence 14767, A
Sequence 2709, Ap
Sequence 13515, A

16 1841.5 37.9 934 14 US-10-369-845-13
17 1834.5 37.8 934 14 US-10-109-791A-277
18 1773.5 36.5 532 12 US-10-425-114-42582
19 1766.5 36.4 931 15 US-10-369-493-3873
20 1605 33.0 956 14 US-10-109-791A-129
21 1571 32.3 964 15 US-10-369-493-2022
22 1571 32.3 966 14 US-10-109-791A-37
23 1571 32.3 966 14 US-10-109-791A-65
24 1565 32.2 966 14 US-10-109-791A-125
25 1564 32.2 966 14 US-10-109-791A-172
26 1561 32.1 966 14 US-10-109-791A-124
27 1424.5 29.3 350 12 US-10-424-599-284633
28 1078.5 22.2 849 15 US-10-369-493-4999
29 880 18.1 841 15 US-10-369-493-11322
30 824 17.0 533 15 US-10-369-493-12632
31 814 16.8 842 15 US-10-369-493-9740
32 803.5 16.5 851 12 US-10-282-122A-74805
33 799.5 16.5 869 15 US-10-369-493-19983
34 797.5 16.4 872 9 US-09-815-242-12333
35 796.5 16.4 871 9 US-09-815-242-5274
36 793.5 16.3 774 12 US-10-282-122A-44374
37 792.5 16.3 877 12 US-10-282-122A-70970
38 791.5 16.3 888 15 US-10-369-493-11784
39 790.5 16.3 849 12 US-10-282-122A-72450
40 786 16.2 869 12 US-10-282-122A-51818
41 785 16.2 932 12 US-10-282-122A-52510
42 785 16.2 949 12 US-10-282-122A-53164
43 782.5 16.1 893 15 US-10-369-493-14767
44 780 16.1 912 15 US-10-369-493-2709
45 778.5 16.0 844 9 US-09-815-242-13515

QY 181 FTLNLSALVAGCRECLVPAETGKSSEYRPMFPAISRCGVWVTERKKTFFKGRDLVQDLG 240
 DB 181 FTLNLSALVAGCRECLVPAETGKSSEYRPMFPAISRCGVWVTERKKTFFKGRDLVQDLG 240
 QY 241 RLKVGSEVPVRLVSGFECASGALGCIISYAEALLADESNYNTYKQYNLNSYMLDSAA 300
 DB 241 RLKVGSEVPVRLVSGFECASGALGCIISYAEALLADESNYNTYKQYNLNSYMLDSAA 300
 QY 301 MRALNVMESKSDANKNFSLFGLMNRCTAGMGKRLHMLWKOPLLDVEEINCRDLVQSF 360
 DB 301 MRALNVMESKSDANKNFSLFGLMNRCTAGMGKRLHMLWKOPLLDVEEINCRDLVQSF 360
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 DB 361 VEDAALRODLRQHLKRIISDIERLTHNLERKRASLVHVVKLYQSSTRVPYIKSVLERHDGQ 420
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 DB 421 FTLNLSALVAGCRECLVPAETGKSSEYRPMFPAISRCGVWVTERKKTFFKGRDLVQDLG 240
 QY 481 FTLNLSALVAGCRECLVPAETGKSSEYRPMFPAISRCGVWVTERKKTFFKGRDLVQDLG 240
 DB 481 FTLNLSALVAGCRECLVPAETGKSSEYRPMFPAISRCGVWVTERKKTFFKGRDLVQDLG 240
 QY 541 FTLNLSALVAGCRECLVPAETGKSSEYRPMFPAISRCGVWVTERKKTFFKGRDLVQDLG 240
 DB 541 FTLNLSALVAGCRECLVPAETGKSSEYRPMFPAISRCGVWVTERKKTFFKGRDLVQDLG 240
 QY 601 FTLNLSALVAGCRECLVPAETGKSSEYRPMFPAISRCGVWVTERKKTFFKGRDLVQDLG 240
 DB 601 FTLNLSALVAGCRECLVPAETGKSSEYRPMFPAISRCGVWVTERKKTFFKGRDLVQDLG 240
 QY 661 FTLNLSALVAGCRECLVPAETGKSSEYRPMFPAISRCGVWVTERKKTFFKGRDLVQDLG 240
 DB 661 FTLNLSALVAGCRECLVPAETGKSSEYRPMFPAISRCGVWVTERKKTFFKGRDLVQDLG 240
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 DB 841 FTLNLSALVAGCRECLVPAETGKSSEYRPMFPAISRCGVWVTERKKTFFKGRDLVQDLG 240
 QY 901 FTLNLSALVAGCRECLVPAETGKSSEYRPMFPAISRCGVWVTERKKTFFKGRDLVQDLG 240
 DB 901 FTLNLSALVAGCRECLVPAETGKSSEYRPMFPAISRCGVWVTERKKTFFKGRDLVQDLG 240

RESULT 2

US-10-029-065-4
 ; Sequence 4, Application US/10029065
 ; Publication No. US20030150024A1
 ; GENERAL INFORMATION:
 ; APPLICANT: May, Gregory
 ; APPLICANT: Baszcyński, Christopher
 ; APPLICANT: Zhu, Tong
 ; APPLICANT: Kipp, Peter
 ; APPLICANT: Mahajan, Pranod
 ; TITLE OF INVENTION: PLANT MSH2 SEQUENCES AND METHODS OF USE
 ; FILE REFERENCE: 5939-2 (035839/196219)
 ; CURRENT APPLICATION NUMBER: US/10/029, 065
 ; CURRENT FILING DATE: 2001-12-20
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 939
 ; TYPE: PRT
 ; ORGANISM: Nicotiana tabacum

US-10-029-065-4
 Query Match 99.9%; Score 4856; DB 14; Length 939;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 938; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNELEQSKLPELKLDAKQAGFLSPFKTLKPKDPAVRVLPDRDYITSHGDDATFIAET 60
 DB 1 MNELEQSKLPELKLDAKQAGFLSPFKTLKPKDPAVRVLPDRDYITSHGDDATFIAET 60
 QY 61 YYHTTALRQGNRADALSSVSERNPFETIARDILLERMDRTILEYEGSGSNMRLVKS 120
 DB 61 YYHTTALRQGNRADALSSVSERNPFETIARDILLERMDRTILEYEGSGSNMRLVKS 120
 QY 121 TPGNLGSPEDILFANNEMONSPTAALAPNGQCEVGLGVYDITKVLGITTEFLDUSH 180
 DB 121 TPGNLGSPEDILFANNEMONSPTAALAPNGQCEVGLGVYDITKVLGITTEFLDUSH 180
 QY 181 FTLNLSALVAGCRECLVPAETGKSSEYRPMFPAISRCGVWVTERKKTFFKGRDLVQDLG 240
 DB 181 FTLNLSALVAGCRECLVPAETGKSSEYRPMFPAISRCGVWVTERKKTFFKGRDLVQDLG 240
 QY 241 RLKVGSEVPVRLVSGFECASGALGCIISYAEALLADESNYNTYKQYNLNSYMLDSAA 300
 DB 241 RLKVGSEVPVRLVSGFECASGALGCIISYAEALLADESNYNTYKQYNLNSYMLDSAA 300
 QY 301 MRALNVMESKSDANKNFSLFGLMNRCTAGMGKRLHMLWKOPLLDVEEINCRDLVQSF 360
 DB 301 MRALNVMESKSDANKNFSLFGLMNRCTAGMGKRLHMLWKOPLLDVEEINCRDLVQSF 360
 QY 361 VEDAALRODLRQHLKRIISDIERLTHNLERKRASLVHVVKLYQSSTRVPYIKSVLERHDGQ 420
 DB 361 VEDAALRODLRQHLKRIISDIERLTHNLERKRASLVHVVKLYQSSTRVPYIKSVLERHDGQ 420
 QY 421 FTLNLSALVAGCRECLVPAETGKSSEYRPMFPAISRCGVWVTERKKTFFKGRDLVQDLG 240
 DB 421 FTLNLSALVAGCRECLVPAETGKSSEYRPMFPAISRCGVWVTERKKTFFKGRDLVQDLG 240
 QY 481 FTLNLSALVAGCRECLVPAETGKSSEYRPMFPAISRCGVWVTERKKTFFKGRDLVQDLG 240
 DB 481 FTLNLSALVAGCRECLVPAETGKSSEYRPMFPAISRCGVWVTERKKTFFKGRDLVQDLG 240
 QY 541 FTLNLSALVAGCRECLVPAETGKSSEYRPMFPAISRCGVWVTERKKTFFKGRDLVQDLG 240
 DB 541 FTLNLSALVAGCRECLVPAETGKSSEYRPMFPAISRCGVWVTERKKTFFKGRDLVQDLG 240
 QY 601 FTLNLSALVAGCRECLVPAETGKSSEYRPMFPAISRCGVWVTERKKTFFKGRDLVQDLG 240
 DB 601 FTLNLSALVAGCRECLVPAETGKSSEYRPMFPAISRCGVWVTERKKTFFKGRDLVQDLG 240
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RESULT 3

US-10-270-839-49

Sequence 49, Application US/10270839
Publication No. US20030143586A1
GENERAL INFORMATION:
APPLICANT: Chao, Qimin
APPLICANT: Grasso, Luigi
APPLICANT: Sassi, Philip M.
APPLICANT: Nicolaides, Nicholas C.
TITLE OF INVENTION: Genetic Hypermutability of Plants for Gene Discovery and Diagnosis
FILE REFERENCE: AG000205 (MOR-0133)
CURRENT APPLICATION NUMBER: US/10/270,839
CURRENT FILING DATE: 2002-10-11
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn version 3.1
SEQ ID NO 49
LENGTH: 937
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-270-839-49

Query Match 74.7%; Score 3629; DB 14; Length 937;
Best Local Similarity 72.4%; Pred. No. 2.7e-303;
Matches 680; Conservative 137; Mismatches 118; Indels 4; Gaps 3;

Qy 1 MNENLEQSKLPKLDKAKQAGFLSPKTLKDPRAVLEFDRDYTTSHGDDATFIAET 60
Db 1 MEGNFEONKULPELKDQAKQAGFLSPKTLKDPRAVLEFDRDYTTSHGDDATFIAET 60

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Db 61 YYHTTALRQLGSNALSSVSISNNPMTIARDILLERMDRTILEYEGSGNRLVKSG 120

Qy 121 TPGNLGSPEDILFANNEMQNSPVIAALAPNGQNGCEVGLGYVDITKRVGLGTFLDDSH 180
Db 121 SPGNIGSPEDVLFANNEMQNTFVVVISPPSPHDCRCVTGMAYVDLTRVLGLAEFLDDSR 180

Qy 181 FTNLESALVALGCRECLVPATGKSSSRVPMFPAISRCGVVMVTERKTEFKGRDILVDLG 240
Db 181 FTNLESALVALGCEKIPPAESGSKSCKSLYSLERCAVMTERKTEFKGRDILVDLG 240

Qy 241 RLKVGSPVPRDLVSGFPCASGALGCLISYAEILLADESNYNTVKQNLNSYMRDLSAA 300
Db 241 RLKVGSPVPRDLVSGFPLATFALGALLSPFELLSDNEDYGNFIRRYDIGFWRDLSAA 300

Qy 301 MRALNVESKSDANKNFSLFGIMNRTCTAGMGKRLHMLKQPLLDVBEINCRDLVQSF 360
Db 301 MRALNVESKTDANKNFSLFGIMNRTCTAGMGKRLHMLKQPLVDLNEIKTRLDIVQCF 360

Qy 361 VEDAAALRODLRHLKRIISDIERLTHNLERKASLVHVVKYQSSSTRVPIKSVLERHDGQ 420
Db 361 VEEAGRLQDLRHLKRIISDIERLTHNLERKASLVHVVKYQSSSTRVPIKSVLERHDGQ 420

Qy 421 PATLIRIYIDSLKWSDDNHLNPIGLVETSVLDLQLENGEYMISSAYDPNLSALKDQK 480
Db 421 PASLISERYLKLKLEALSQDHLGKFDLVECSVDLDLQLENGEYMISSAYDPNLSALKDQK 480

Qy 481 ETLERQIHLKHQTANDLIDLPIDKSLKLDKTOFGHVFRIITKKEPKVKRQKLNHSHYVLE 540
Db 481 ELLEQQIHELKHKTAEIDLDVQKALKLDKAAQFGHVFRIITKKEPKVKRQKLNHSHYVLE 540

Qy 541 TRKQGVKFTYTKLKLQDQFQKIVVEYKSCOKELVARVQVTAASFSRVFAGIAGVLAELD 600
Db 541 TRKQGVKFTYTKLKLQDQFQKIVVEYKSCOKELVARVQVTAASFSRVFAGIAGVLAELD 600

Qy 601 VLLSPADLAASCTPYTRFNISPPDTGDIILEGCRHPCVEAQDWNSIPNDCRLVRGESW 660
Db 601 VLLSPADLAASCTPYTRFNISPPDTGDIILEGCRHPCVEAQDWNSIPNDCRLVRGESW 660

Qy 661 FOITGPNMGKSTVIROGVNVLMAQVGSFVPCDNALISIRDCIFARVAGDQCQLRGVS 720
Db 661 FOITGPNMGKSTVIROGVNVLMAQVGSFVPCDNALISIRDCIFARVAGDQCQLRGVS 720

Qy 721 TFMQEMLETASILKGATDRSLIIIDELGRGTSTYDGFGLAWAICHEHIVEIKAPTLFATH 780
Db 721 TFMQEMLETASILKGATDRSLIIIDELGRGTSTYDGFGLAWAICHEHIVEIKAPTLFATH 780

Qy 781 FHELTALANKGD-NGHKKAGIANFVFAHIDPSNRKLTMLYKVPKACDQSGFIHVAE 839
Db 781 FHELTALQAQANSEVSGN-TVGVANFVSAHIDPESRKLTMLYKVPKACDQSGFIHVAE 838

Qy 840 FANPPPSVVALAREKASELDEDFSIPIIPNDIKEAASKRKEFDEHDSVSGTARQFLO 899
Db 839 FANPPESVVALAREKAAAELEDFSSMIINN-ESGKRKSGREDDPDEVSGAERAHFLK 897

Qy 900 DFAQLPLDKDENVVRKLSKMTDLERDAVDSHLQOF 938
Db 898 EFAAMPDLKMLKDSLQVRKMDLEKDAADCHWLQOF 936

RESULT 4
US-10-425-114-56470
Sequence 56470, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 56470
LENGTH: 860
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: UC-ZMFLB73219B02_FLI.pep
US-10-425-114-56470

Query Match 63.4%; Score 3082.5; DB 12; Length 860;
Best Local Similarity 68.4%; Pred. No. 3.1e-256;
Matches 588; Conservative 119; Mismatches 150; Indels 3; Gaps 3;

Qy 82 SVSRNMFETIARDILLERMDRTILEYEGSGNRLVKSGTGNLGSFEDILFANNEMQNS 141
Db 2 SVSKAMPETIARNILLERTCTLELYEGSGNRLVKSGTGNLGSFEDILFANNEMQNS 61

Qy 142 PVIAALAPNGQNGCEVGLGYVDITKRVGLGTFLDDSHFTNLESALVALGCRECLVPAE 201
Db 62 PVIALPFPACRESQLYVGLSFLDMNRLKGLAEFPDSRFTNVESALVALGCKECLLPAD 121

Qy 202 TGKSEYRPMFPAISRCGVVMVTERKTEFKGRDILVDLQGLRVKGSVEPVRDLVSGFECAS 261
Db 122 CEKSIDLNPLODVISNCNVLITKSKADFKSRDLAQDLGRIIRGVSVEPVRDLVSGFDVAL 181

Qy 262 GALSCLISYAEILLADESNYNTVKQNLNSYMRIDSAAMPALNVMSKSDANKNFSLFG 321
Db 182 GPLGALLSYAEILLADDTNYGNTTETKYNLNCYMRDLSAAVRAALNIAEGKTQVNFSLFG 241

Qy 322 LMNFTCTAGMKRLHMLKQPLLDVBEINCRDLVQSFVEDAALRODLRHLKRIISDIE 381
Db 242 LMNFTCTAGMKRLHMLKQPLLDVBEINCRDLVQSFVEDAALRODLRHLKRIISDIE 301

Qy 382 RLTHNLERKASLVHVVKYQSSSTRVPIKSVLERHDGQFATLIRIYIDSLKWSDDNH 441
Db 302 RLTHNLERKASLVHVVKYQSSSTRVPIKSVLERHDGQFATLIRIYIDSLKWSDDNH 361

Qy 442 LNKFIGLIVETSVLDLQLENGEYMISSAYDPNLSALKDQKLEQIHLKHQTANDLIDLP 501
Db 362 FGRFSSSLVETAIADLAQLENGEYRISPLYSSDLGVLKDELSVVENHNLHVDITASDLDLS 421

QY	502	IKSKLKDKETQFGVHFRITKKEPKVKRQKLNSHYIVLETRKDGVKFTYTKLKLGDQFQ	561
Db	422	VDKQLKLEKGS-LGHVFRMSKKEQKVRKKLTGSGYIIITRKDGVKFTNSKLNLSDOYQ	480
QY	562	KIVREYKSCOKELVARVVOTAASSEVPAGIAGVLAEVLDSFADLAASCPPTPRPNI	621
Db	481	ALFGEYTSCKVKVGVDDVVRSVGTSEVFENFAVLSELDVLQSFADLAATSCVPVVRPDI	540
QY	622	SPPTGDIILGCRHPCVEAQDWNSIPNDCLVRGESWFOIITGNMGCKSTYTRQGVV	681
Db	541	TASDEGDIVLGSRHPCLEAQDGVNFI PNDCITLVRGKSWFOIITGNMGCKSTYTRQGVV	600
QY	682	NVLMAQVGSFPCDNATISIRDCIFARVAGDCQCLRGVSTFMQEMLETASILKGATDRSL	741
Db	601	NVLMAQVGSFVPCDAQSISVRDCIFARVAGDCQLHGVSTFMQEMLETASILKGASDKSL	660
QY	742	IIIDELGRGTSYTGFGLAWEI CBIHVEEIKAPTLFATHEHILTALANKGD-NGHKNA	800
Db	661	IIIDELGRGTSYTGFGLAWEI CBIHVEEIVTRAPTLFATHEHILTALAHNRNDEHQHISDI	720
QY	801	GIANPHVFAHIDPNSNRKLTMLYKVHPGACDQSGFIHVAAEFANPPSPVALAREKASELED	860
Db	721	GVANHVGAHIDPLSRKLTMLYKVHPGACDQSGFIHVAAEFANPPFAVVALAKSAELED	780
QY	861	FSPIAIIPNDIK-EAASKKEEFDRHVSRCBARQFLODFALPLDKMDPNVVRQKLS	919
Db	781	FSTFTTFSDDLKDEVGSKRKRVSPDDITRGAARARUFLFEFALPMDMDGSKILEMAT	840
QY	920	KMKTDLERDAVDSHWLQOFF	939
Db	841	KMKADLQKDAADNPWLQOFF	860

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RESULT 5
US-10-424-599-214104
; Sequence 214104, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovacic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 214104
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_35361C.1.pep
US-10-424-599-214104

```

	Query Match.	48.5%;	Score 2358;	DB 12;	Length 592;
	Best Local Similarity	76.0%;	Pred. No. 4.9e-194;		
	Matches 449;	Conservative 68;	Mismatches 72;	Indels 2;	Gaps 2;
Qy	350	INCELDIVQSFVEDAALRODLRQHLKKSIDTERTLNLERKRASLVHVVKLYQSSSTVPPY	409		
Db	1	INSLDLIVQAFVEDTALRQDLRQHLKRISDTERLMLNIQKRRLGLOHIVKLVQYSILPPY	60		
Qy	410	IKSVLRHDDGQFATLIERVYIDSLSEKWSDDNHLNKFGLVETSDVLDQLENGEYMISSAY	469		
Db	61	IKSALERYDGGQFSTPMRSRYLEPIELWTDDHNLNKFGLVEASVDLDQLENREYMISSPY	120		
Qy	470	DPNLSALKDQEQETLERQIHNLHKQTANDLDPIDKSLKLDKETQFGHVFRITKKKEPKVR	529		
Db	121	DSILANIKDQOELESQI ONLHROTADDLPMPKALKL DGTGFGHVFRITKKKEPKIR	180		

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530 QY KQNSHYVLETRKDGVKFTYTKLKGDDQFKIVIEYKSCQKELVARVWQTAAFSSEVF 589
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
181 Db KKLNTQFIIILETRKDGVKFTNTKLKLGDDQYQOILEYKSCQKLVDRVWQTAAFTSEVF 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
590 QY AGIAGVLAELDVLLSPADLAASCTPYTRNIGSPDDGDIILEGCRHPCVEAQDWNSIP 649
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
241 Db ESUREIISLVDVLLSPADLAASSCTPYTRPDITSSDEGDIILEGCRHPCVEAQDWNVFIP 300
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
650 QY NDCRLVGRGSEWFOIITGPNNGGKSTYIRQGVNVLMVAQGVSPVPCDNATISIRDCIFARV 709
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
301 Db NDCKLVGRGTWFQIITGPNNGGKSTFIRQGVNITMAQGVSPVPCDNASISVRDCIFARV 360
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
710 QY GAGDCOLRGVSTFMQEMLETFASILKGATDRSLIIIDELGRGTSTYDQGLAWAJCEHIVE 769
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
361 Db GAGDCOLRGVSTFMQEMLETFASILKGATDKSLIIIDELGRGTSTYDQGLAWAJCEHIVE 420
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
770 QY EIKAPTILFATHHELTALANKNGDNGHKCN-AGIANPHVFAHIDPSNRKLTMLYKVHPGA 828
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
421 Db VIKAPTILFATHHELTALALEVNSDQKQIVGVNHYVSHIIDSSTKLTMLYKVPEGA 480
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
829 QY CDQSGFIHVAEFANPPSPVVALAREKASELEDFSPIAL-IPNDIKEASKRKRFDRHDV 887
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
481 Db CDQSGFIHVAEFANPPSPVTLAREKAAELEDFPSATSLNHTTQEVGSKRKRAPEPDDM 540
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
888 QY SRGTARARQLOPFAQLPLDKMDENVVRQKLSMKMTDLERDAVDSHNLQQF 938
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
541 Db SQGAARARQLEAFVALPLETMDKQVALQEVKKLTDTLEKDAENCNWLOQF 591
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
US-10-425-114-45750
; Sequence 45750, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 45750
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 701182994_FLI.pep
US-10-425-114-45750

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	Query Match	41.3%;	Score 2004.5;	DB 12;	Length 567;
	Best Local Similarity	67.3%;	Pred. No. 1.4e-163;		
	Matches 382;	Conservative 80;	Mismatches 103;	Indels 3;	Gaps 3;
Qy	374	LKRISDIERLTHNLKRASLVHWVKLYQSSTVPYIKSVLERHDGQFATLIRERYIDSL	433		
Db	1	LKRISDLDRUTHSLRKKSANLQPVVKLYQCSRIPIYIKGLQQYNGQFSLIRSKFLEPL	60		
Qy	434	EKWSDDNHLNKFGLVETSVLDLQLENGEYMWISAYDPNLSALKDEQETLERQIHNLHKQ	493		
Db	61	EENWAKNRFGRFSLSVETALDLAQLENGEXYRISPLYSDDLGVLKDELSVVENHNNLHVD	120		
Qy	494	TANDLDLPIDKSLDKDETQGHVERITTKKEEPPKVRKQLNSHYIVLRETRKDGQVKTFTKL	553		
Db	121	TASDLDDVSUDQKULEKGS-LGHVFRNKKKEEQQKVRKLLTGSVLIIVRETRKDGQVKTFTSKL	179		
Qy	554	KGLGDQFQKITYEYKSCQKELVARVVQTAASFSEVFAGIAGVLAEVDVLVSFADLAASCP	613		
Db	180	KNLSDYQALFGETSCOKKVGVDVRVSGTTFSEVFENFAVLSELQVQSADLATSQCP	239		

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QY 614 TPYRPNISPDGDIIEGCRHPCVQAQWNSIPNDCLVRGSEWFOIITGNMGSKS 673
Db 240 VPYVRPDITASDEGIVLLSRHPCLBAQGWFIPIPDCTIVRGKSWFOIITGNMGSKS 299
QY 674 TYIRQGVNVVMAQVGFVPCDNATISIRDCIFARVAGAGCQGLRGVSTFMQEMLETSIL 733
Db 300 TFIRQGVNVVMAQVGFVPCDNATISIRDCIFARVAGAGCQGLRGVSTFMQEMLETSIL 359
QY 734 KGATDRSLIILDELGRGTSYDGGFLAWACEHIVEIKAPTLFATHFELTALANXGD 793
Db 360 KGASDKSLIILDELGRGTSYDGGFLAWACEHIMEVTRAPTLFATHFELTALAHREND 419
QY 794 -NGHKKNAGIANFHVFAHIDPSNRKLTMLYKVHPGACDQGFHIVAGFANFPSPVALAR 852
Db 420 EQHISIDIGVANHVGAIIDPLSKLTMLYKVHPGACDQGFHIVAGFANFPSPVALAK 479
QY 853 EKASELEDFSPALIPNDIK-EAASKRREDFRDHVSRGRTARAFQIQQDPAQLDKMDP 911
Db 480 SKAAELEDFTTPTFSDDLKDEVGSKRKFVSPDDITRGAARARLFEEFAALPMDEMDG 539
QY 912 NVVRQKLSKMKTLERDAVSHWLOQFF 939
Db 540 SKILEMATKMKADLQKDAADNPMLQOFF 567

RESULT 7
US-10-109-791A-66
; Sequence 66, Application US/10109791A
; Publication No. US2003013878A1
; GENERAL INFORMATION:
; APPLICANT: Biotech Oncologic Corp.
; TITLE OF INVENTION: Functional Genetic Tests of DNA Mismatch Repair
; FILE REFERENCE: EPOL 102 NP
; CURRENT APPLICATION NUMBER: US/10/109,791A
; CURRENT FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 934
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-109-791A-66

```

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Query Match 37.9%; Score 1842.5; DB 14; Length 934;
Best Local Similarity 43.0%; Pred. No. 2.9e-149; Mismatches 307; Indels 55; Gaps 19;
Matches 403; Conservative 172;

QY 14 LKLDKAOAGFLSFFKTLPKDP-RAVRLFRDRDYTTSHGDDATFIATYTHHTTALRQLG 72
Db 9 LQESAAEVGFVRFQGMPEKPTTTLVLRDGRDFTAHGEDALLAAREVFKTGVIKYM 68

QY 73 NR-ADALSSVSERNMPTETARDILLERMORTLELYEGGSN-----WRLVKSCTPGN 124
Db 69 PAGAKNLSQVLSKMNPSFVSKOLLVRYR-VEVYKRNAGNKASKENDWYLAJKASPGN 127

QY 125 LGSFEDILFANNMONSPVIAALAPNGQNGCEVLGVVDITKRVGLGTBFLDDSHFTNL 184
Db 128 LSQFEDILFGNDSAGISGVGVKMSAVDQGVGVVDSIQKGLGCEFPDNDQFNSL 187

QY 185 ESALVALGCRECLVP-AET-GKSSEYRPMFDAISRCGMVMTERRKTKFKGRDLVQDLGRL 242
Db 188 EALLIQIGPKECVLPGETAGDMGKLAQI---IQRGILITERKKADFTKDIYQDLNRL 244

QY 243 VKG-----SVEPVRDLVSGFCASGALGCLISYAEILLADESNYQNTYKQVNLNSYM 294
Db 245 LKGGKKGQMSAVLPENE---NQVAVSSLSAVIKFLELLSDSDSNFQGFELTTDFDSQYM 300

QY 295 RLDSAAARALNVME-SKSDANKFSLGLMNRCTCTAGMKRLHMLKQPLLDVVEINCR 353
Db 301 KLDIAARALNLFQGSVEDTDSLSAALINK-CKTPQGRVLNVQWIKQPLMDKNRLEER 359

QY 354 LDLVQSFVEDAALRQDLRQH-LKRISDIERTLTHNLERKRASLVHVVKLYQSSTRVPYIKS 412

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Db 360 LNLVEAFVEDAELRQTLQEDLLRRFPDLNRLAKKFFQQAANLQDCYELYQINQLPNVIQ 419
QY 413 VLERHQQFATLIRERYIDSLKWSDDNHLNKIFGLVETSVDDOLENGEYMISSADPN 472
Db 420 ALEKHEGKHOKLLAVFVPTPLTLDRSD--FSKEQEMIEITLMDQVENHEFLVKPSPDPN 477
QY 473 LSAKDQEQETLQRIHNLHKQTANDLPLDKSLDKDKETQFGHVRI TKKEEPKVKQL 532
Db 478 LSELRIMNDLEKXOMOSTLISAARDIGLDPKQIKLDSSAQFGYFFVTKCKEKKVLRN-- 535
QY 533 NSHYIVLETRKDGKVTYTKLKLGGQFQKIVVEYKSCQKELVARVVQTAASFSEVFAI 592
Db 536 KNFSTVDIQKNGVKFTNSKLTSLNEEYTKNTEYBEAQDAIVKEIVNISSGVVEPMQTL 595
QY 593 AGVLAELDVLLSPADLAASCPPTYTPNPISPPDTGDIILEGCRHPCVQAQWNSIPND 652
Db 596 NDVLAQLDAVVSFAHVSNGAPVFPVFAILEKQGRILKASRHACVEVQDEIAFIENDV 655
QY 653 RLVRGESWFOIITGNMGKSTYIRQGVNVMAQVGFVPCDNATISIRDCIFARVAG 712
Db 656 YFEKDKQMFHIIIGPNMGKSTYIRQGVNVMAQVGFVPCDNATISIRDCIFARVAG 715
QY 713 DCQLRGVSTFMQEMLETSILKGTATDRSLIILDELGRGTSYDGGFLAWACEHIVEIK 772
Db 716 DSQKGVSTFMAEMLETSILRSATKDSLIIIDELGRGTSYDGGFLAWAISEVIATKIG 775
QY 773 APTLFPATHFELTALANXGDNGHKKNAGIANFHVFAHIDPSNRKLTMLYKVHPGACDQ 832
Db 776 AFCMFATHFELTALAN-----QIPVNNLHVTL--TTBETTLMLYQVKKGVCDQS 825
QY 833 FGHVAFANFPSPVALAREKASELEDFSPALIPN-DIKEAASKR---KREFDRHDVS 888
Db 826 FGHVAFANFPSPVALAREKASELEDFSPALIPN-DIKEAASKR---KREFDRHDVS 888
QY 889 RGTARARQFLQDPAQLDKMDPNVVRQKLSKMKTDL 925
Db 879 QGKIKQEFSLKVKQMPFTEMSSEENITIKLQKLAEV 915

RESULT 8
US-09-788-657-19
; Sequence 19, Application US/09788657
; Patent No. US20020123149A1
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas
; APPLICANT: Sassi, Philip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Grasso, Luigi
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Methods for generating hypermutable
; TITLE OF INVENTION: yeast
; FILE REFERENCE: 01107.00097
; CURRENT APPLICATION NUMBER: US/09/788,657
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,336
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 934
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-657-19

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Query Match 37.9%; Score 1841.5; DB 9; Length 934;
Best Local Similarity 43.0%; Pred. No. 3.6e-149;
Matches 403; Conservative 172; Mismatches 307; Indels 55; Gaps 19;

QY 14 LKLDKAOAGFLSFFKTLPKDP-RAVRLFRDRDYTTSHGDDATFIATYTHHTTALRQLG 72
Db 9 LQESAAEVGFVRFQGMPEKPTTTLVLRDGRDFTAHGEDALLAAREVFKTGVIKYM 68

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QY	73	NR-ADALSSYSVGRNMFETIARDILLERMORTLELYEGSGSN-----WRLVKSGTGPEN	124
Db	69	PAGAKNLQSVLTKQNFESFVKOLLIVRQYR-VEVYKRNAGNKASKENDWYLYAKSPGN	127
QY	125	LGSFEDILLFANNQNSPVTAALAPNFQNGCEVGLGVYDITTKVGLGLTEFLDDSHFTNL	184
Db	128	LSQFEDILFGNNDMSAGISGVGVGPKMSAVDGRQVGVGVYDSIQKGLGLCEFPDNDQSNL	187
QY	185	ESALVALGCRECLYP-AET-GKSSEYRPMFDALSRGVMVTERKKTBFKGBDLVODLGR	242
Db	188	EALLIQIPRECVLPGETAGDMKLRQI---IQGGILITERKADFSTMDIYQDLNRL	244
QY	243	VKG-----SVEPRDLVSGPECASGALCILSYAELLADESNYNTYKQYNLNSYM	294
Db	245	LKGGKQGMNSAVLPEME-----NOVAVSSLSAVIKFLELLSDSNFGGFEUTTFDFSQY	300
QY	295	RLDAAARALNMBE-SKSDANKNFSLFGLMNRCTAGMGKLLHMLWKQLPLLDVEEINCR	353
Db	301	KLDIAAVRALNLFQGSVEDTTGQSALALLNK-CKTPQGRVLVQWIKQPLMDKNRIBER	359
QY	354	LDLVQSFVEDAALRODLRQH-LKLSIDIERLTHNLERKGRASLVHVVKLYQOSTRVPYIKS	412
Db	360	LNLYEAFVEDAEALRQTLQEDLLRRFPDLNRLAKKPFQQAANLQDCRYLYQGINOLPNVIQ	419
QY	413	VLRHGDGFATLIRERYIDSLEKNSDDNHLNKFGLGVETSDLOLENGEYMIISAYDEN	472
Db	420	ALEKHEGKHQKLLANVFVTPLTDLRSD--FSKFQEMIETTLDMQOVENHEFLVKPSFDPN	477
QY	473	LSALKQDBOETLEROJHNLKOTANDLDPIDKSLKLDKETQFQGHVFRITKKEEKPVRKQL	532
Db	478	LSELREIMNDLEKKMQSFTLISAARDLGDGPKQIKLDSAQFGYFYFRVTCKEEKVLRN--	535
QY	533	NSHYVLBTRKDGKVFYTKLKLGDQOKIVEEYKSCQKELVARVWOTAASFSEVFAGI	592
Db	536	NKNFSTVDIQNGVKFTNSKLTSLNEEYTKNTEYEEAQDALVKEIVMISSGYVEPMQTL	595
QY	593	AGVLAELDVLLSFADLAASCPTPYTRPNISPDTCGDIILEGGRHPCVBAQDWVNSIPNDC	652
Db	596	NDVLAQLDAVVSFAHVSNGAPVPYVRPAILEKGQGRILKASRHACVEYQDEIAFIPNDV	655
QY	653	RLVRGESHFQIITGNMGKSHYIRQVGVNVLMAQVSPVPCDNATISIRDCIFARVCGAG	712
Db	656	YFEKDKQMFHIIITGNMGKSTYIRQTVGVILMAQICFVPCESAESVLVDCILARVAG	715
QY	713	DCQLRGVSTFMOEMLETASILKGATDRSLIIDEELGRGTSTYDGRGLAWAICEHIVEEIK	772
Db	716	DSQLKGVSTFMAEMLETASILRSATKDSLIIIDEELGRGTSTYDGRGLAWAISEYIATKIG	775
QY	773	APTLFATHFHELITALKNGDNGHKKNAGIANFHVFAHIDPSNRKLTMLYKYVHPGACDOS	832
Db	776	AFCMFATHFHELITALN-----QIPVNNLHVTL--TTTEETLTMLYQYKKGVCDOOS	825
QY	833	FGIHWAEANFPSPVVALAREKASLEDFSPAIATPN-DIKEAASKR---KEEFORHDVS	888
Db	826	FGIHWAEALANFPKHVIECAKQALALEEFOYIGESQGYDIMEPAACKVYLERE-----	878
QY	889	RGTAARQFLODPAQLPLDKMDPNVVRQKLSKOKTDL	925
Db	879	OGEKIIOEPLSKVKOMPFTMESEENITIKLKOLKAEV	915

RESULT 9
US-09-912-697-10
; Sequence 10, Application US/09912697
; Publication No. US20030068808A1
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas C
; APPLICANT: Sass, Philip M
; APPLICANT: Grasso, Luigi M
; APPLICANT: Kline, J Bradford
; TITLE OF INVENTION: METHODS FOR GENERATING ANTIBIOTIC RESISTANT MICROBES AND NOVEL
; TITLE OF INVENTION: ANTIBIOTICS
; FILE REFERENCE: MOR-0040

```

; CURRENT APPLICATION NUMBER: US/09/912,697
; CURRENT Filing DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 934
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-697-10

Query Match          37.9%; Score 1841.5; DB 10; Length 934;
Best Local Similarity 43.0%; Pred. No. 3.6e-149;
Matches 403; Conservative 172; Mismatches 307; Indels 55; Gaps 19;

QY 14 LKLDAKQAQGLSFFKTLKCPD-RAVRLPDRDYVYTHSGDDAFIARTYVYHTTTALROLG 72
DB 9 LQLESAAEYVFEFFQPMPEKPTTVRLFRGDFYTAHGEDALLAAREVFTQGVIKVMG 68
QY 73 NR-ADALSSVSVRNPFETIARDILLERMORTILEYEGSGSN-----WRLVKSGTTPGN 124
DB 69 PAGAKNLQSVLTKMNFESFVKDLLVRQYR-VEVYKNRAGNASKASKENDWVLYAKASFGN 127
QY 125 LGSFEDILFANNEMQNSPVIAALAPNPGQNGCEVLGYVDITKRVLGCTFEFLDDSHETNL 184
DB 128 LSQFEDILFGNNDMSASIGVVGVKMSAVDQQRQGVGYVDSIQKGLGCLCFPPDMNDQFSNL 187
QY 185 ESALVAGCRECLVP-AET-GKSEYRPMEDATSRCGVMVTERKTKTEFKGRDLVQDGLRL 242
DB 188 EALLIQGPKECVLPGETAGDMKGLRQI---TQGGILLTERKADFSTKDIYQDLNRL 244
QY 243 VKG-----SVEPVRDLVSGFECASGALGCILSYAELIADENSNGYTVKQVNLNSYM 294
DB 245 LKGGKKGQOMNSAVLPENE---NQVAVSSLSAVIKFLELLSDSSNFQGFELTTDFDSQYM 300
QY 295 RLDSAAARALNVME-SKSDANKNFSLRGLMNRCTACMGKRLHMLWKLOPLLDVEENCR 353
DB 301 KLDIAAARALNLPQGSVEDTTGSOSLAALNKK-CKTPOGRLVNQWIKQPLMDKNRTEER 359
QY 354 LDLVQSFEVDEAALRQDLRQH-LKRISDIERLTHNLKRASLHVHVVKLYQSGSTVPYIKS 412
DB 360 LNLVEAFVEDAEALRQLTQEDLLRRFPDLNRLAKKFRQQAANLQCYRLYQGINLPNVIQ 419
QY 413 VLERHGDQFATLIRERVYDSLEKWSDDNHLNKFGLVETSVDDLQLENGEYMWISSADPN 472
DB 420 ALEXHEGKHQKLLAVFVPTLDRSD--FSKFOEMITETLLDMQOVENHEFLVKSFPDPN 477
QY 473 LSALKDQSETLEROIHNHKTANDLDLPDKSLKDKETQGHVFRITKKEEPRKVRKQL 532
DB 478 LSELRINWDLKKKQKSTLISAARDLGLDPGKQIKLDSAGFYFRVTCKEEKVLNR-- 535
QY 533 NSHYVILETRKDGKVFYTKLKKLGDOFKLIVVEYKSCQKELVARVVTGTAASFSEVPFAGI 592
DB 536 NKNFSTVDIQNGVKFTNSKLTSLNEEYTKNKTBYEAAQDAIVKRIVNISSGYVEPMQTL 595
QY 593 AGVLAELDLVLSRADLAASCPTVTRPMISPPDTGDIILEGRCPCEVAQDWNSIPNDCC 652
DB 596 NDVLAQLDVAVSFAHVSNGAPVVPVRPAILEKGGQRIILKASRHACVEVQDEIAPNDV 655
QY 653 RLVRGESWFQIITGNMGKSTYIRQGVNVYLMVAQVGSFVPCDNATISIRDCIFARVGAG 712
DB 656 YFEKDKQWFHIIITGNMGKSTYIRQTGVIVLMAQIGCFVPCESAESVITDCILARVGAG 715
QY 713 DCOLRGSTTFQOEMLETASILKGNATRSLLIIDELGRGTSYDQGLAWAJCEHIVBEIK 772
DB 716 DSQLKGVSTTFMAEMLETASILRSATKOSLLIIDELGRGTSYDQGLAWAJSEYATKIG 775
QY 773 APTLFAFHFELTALANKNGDNHKKNAAGIAFNHFVFAHIDPSNRKLTMLYKHPGACDQS 832
DB 776 AFCMFATHFELTALAN-----QIFTVANLHVTAL--TTEETLTMLYQVKKGVCDCQS 825
QY 833 FGIHVAEPANFPFSSVVALAREKASELEDFSPIAIPN-DIKEAASKR---KREFDRHDVS 888
DB 826 FGIHVAELANPKHVEICAKOKALEEFOVIGESQGYDIMEPAKKCYLERE----- 878

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; PRIOR APPLICATION NUMBER: 60/358,602
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 5
; LENGTH: 934
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-371-857-5

Query Match      37.9%; Score 1841.5; DB 14; Length 934;
Best Local Similarity 43.0%; Pred. No. 3.6e-149;
Matches 403; Conservative 172; Mismatches 307; Indels 55; Gaps 19;

QY 14 LKLDKAOAQOGLSFFKTLKDP-RAVRLFRDRDYTHSHGDDAFIAETYYHTTALRQLG 72
Db 9 LQESAAEVGFVRFGQPEKPTTVRLFRDGRDYTHSHGDDAFIAETYYHTTALRQLG 68
QY 73 NR-ADALSSVSVSRNMFTIARDILLERMDRTLELYEGSGN-----NRLVKSQGTGPN 124
Db 69 PAGAKNLQSVVLSKMFESFVKOLLVQYR-VVYKNRAGNKASKENDWYLAQKSPGN 127
QY 125 LGSFEDILFANNMNSPVTAAALAPNFGQNGCVGLGYDITKRVGLGLTFELDDSHFTNL 184
Db 128 LSQFEDILFANNMNSPVTAAALAPNFGQNGCVGLGYDITKRVGLGLTFELDDSHFTNL 187
QY 185 ESALVALGCECLVP-AET-GKSEYRPMFDTASRCGVMTYRKKTFKGRDLVQDLGRL 242
Db 188 EALLIQIGPKECVLPGETAGDMGKLRQI---IQRGGLITERKKADEFSTKDIYQDLNRL 244
QY 243 VKG-----SVEPVRLVSGFECASGALGCLISVAELADESNYGNVTVKYNLSYM 294
Db 245 LKGGKQGMNSAVLPENE-----NQAVSSLSAVIKFLELLSDSNFQFELTTFDFQYM 300
QY 295 RLDSAAARALNVM-SEKSDANKNPSFLGLMNRCTAGKRLHMLKQPLLDVEEINCR 353
Db 301 KLDIAAVALNLFQGSVEDTTGQSALALNK-CKTPQGRVYNQWIKQPLMDKNRIEER 359
QY 354 LDIVQSVFEDAAALRQDLRQH-LKRISDIERLTHNLERKASLVHVVKLYQSSRTPVPIKS 412
Db 360 LNLVEAFVEADLQTLQEDLLRRFPDLNRLAKFKQQAANLQCYRLYGQINQLPNVIQ 419
QY 413 VLRRHGOFAFLIRERYIDSLKESDDNHLNKFGLVETSDLDLQNGEVMISAYDPN 472
Db 420 ALEKHGKHQKLLAVFVPTLDRSD--FSKQEMETITLDMQOVNHEFLVKPSPDPN 477
QY 473 LSALKDQFETLERQIHNHKLQATANDLPLDKSLKDKETQFGHVFRTITKEEPKVRKQL 532
Db 478 LSELREIMNDLEKKNQSTLSAARDLGLDPGKQIKLDSQAQFGYFRVTCKEEKVLRN-- 535
QY 533 NSHYIVLETRKQGVKFTYTKLKLQDQFKIVEYKSCQKELVARVQTAASFSEVFAGI 592
Db 536 NKNFSTVDIQNGVKFTNSKLTSLNEEYTKNTEYBEAQDAIVKEIYNISSGYVPEMOTL 595
QY 593 AGVLAELDVLISFADLAASCTPTTRNISPDPDGDILLEGCRHPCVCAEADWNSIPND 652
Db 596 NDVLAQLDAVVSFAHVSNGAPVVRPALEKGGQRIILKASRHACVQDEIAFINDV 655
QY 653 RLVRGSENFQIITGNNGKSTYIRQGVNVLMAQVGSFVPCDNATISIRDCIFARVAG 712
Db 656 YFEKDKMFHITGNMGKSTYIRQGVNVLMAQVGSFVPCDNATISIRDCIFARVAG 715
QY 713 DCQLRGVSTFMEMLTASILKQATDRLSLIILDELGRSTYDGFGLAWALCEHIVEIK 772
Db 716 DSQKGVSTFMEMLTASILKQATDRLSLIILDELGRSTYDGFGLAWALCEHIVEIK 775
QY 773 APTLFATHFELTALANKGNGHKKAGIANGFVFAHIDPSNRKILMYKVPFGACDQS 832
Db 776 AFCHFATHFELTALANKGNGHKKAGIANGFVFAHIDPSNRKILMYKVPFGACDQS 825
QY 833 FGIHVAEPANPPSVVALAREKASELEDFSPATIPN-DIKEASKR---KREFDRHDVS 888
Db 826 FGIHVAELANFPKHFIECAKQALEBFBQVIGBSQGYDIMEPAKCKYLERE----- 878

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RESULT 14

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US-10-371-634-9
; Sequence 9, Application US/10371634
; Publication No. US20030170895A1
; GENERAL INFORMATION:
; APPLICANT: Morphotek Inc.
; APPLICANT: Grasso, Luigi
; APPLICANT: Nicolaides, Nicholas C.
; APPLICANT: Sassi, Philip M.
; TITLE OF INVENTION: Methods of Making Hypermutable Cells Using PMSR Homologs
; FILE REFERENCE: FT0005 US (MOR-0146)
; CURRENT APPLICATION NUMBER: US/10/371,634
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/358,578
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 9
; LENGTH: 934
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-371-634-9

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Query Match      37.9%; Score 1841.5; DB 14; Length 934;
Best Local Similarity 43.0%; Pred. No. 3.6e-149;
Matches 403; Conservative 172; Mismatches 307; Indels 55; Gaps 19;

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QY 14 LKLDKAOAQOGLSFFKTLKDP-RAVRLFRDRDYTHSHGDDAFIAETYYHTTALRQLG 72
Db 9 LQESAAEVGFVRFGQPEKPTTVRLFRDGRDYTHSHGDDAFIAETYYHTTALRQLG 68
QY 73 NR-ADALSSVSVSRNMFTIARDILLERMDRTLELYEGSGN-----NRLVKSQGTGPN 124
Db 69 PAGAKNLQSVVLSKMFESFVKOLLVQYR-VVYKNRAGNKASKENDWYLAQKSPGN 127
QY 125 LGSFEDILFANNMNSPVTAAALAPNFGQNGCVGLGYDITKRVGLGLTFELDDSHFTNL 184
Db 128 LSQFEDILFANNMNSPVTAAALAPNFGQNGCVGLGYDITKRVGLGLTFELDDSHFTNL 187
QY 185 ESALVALGCECLVP-AET-GKSEYRPMFDTASRCGVMTYRKKTFKGRDLVQDLGRL 242
Db 188 EALLIQIGPKECVLPGETAGDMGKLRQI---IQRGGLITERKKADEFSTKDIYQDLNRL 244
QY 243 VKG-----SVEPVRLVSGFECASGALGCLISVAELADESNYGNVTVKYNLSYM 294
Db 245 LKGGKQGMNSAVLPENE-----NQAVSSLSAVIKFLELLSDSNFQFELTTFDFQYM 300
QY 295 RLDSAAARALNVM-SEKSDANKNPSFLGLMNRCTAGKRLHMLKQPLLDVEEINCR 353
Db 301 KLDIAAVALNLFQGSVEDTTGQSALALNK-CKTPQGRVYNQWIKQPLMDKNRIEER 359
QY 354 LDIVQSVFEDAAALRQDLRQH-LKRISDIERLTHNLERKASLVHVVKLYQSSRTPVPIKS 412
Db 360 LNLVEAFVEADLQTLQEDLLRRFPDLNRLAKFKQQAANLQCYRLYGQINQLPNVIQ 419
QY 413 VLRRHGOFAFLIRERYIDSLKESDDNHLNKFGLVETSDLDLQNGEVMISAYDPN 472
Db 420 ALEKHGKHQKLLAVFVPTLDRSD--FSKQEMETITLDMQOVNHEFLVKPSPDPN 477
QY 473 LSALKDQFETLERQIHNHKLQATANDLPLDKSLKDKETQFGHVFRTITKEEPKVRKQL 532
Db 478 LSELREIMNDLEKKNQSTLSAARDLGLDPGKQIKLDSQAQFGYFRVTCKEEKVLRN-- 535
QY 533 NSHYIVLETRKQGVKFTYTKLKLQDQFKIVEYKSCQKELVARVQTAASFSEVFAGI 592
Db 536 NKNFSTVDIQNGVKFTNSKLTSLNEEYTKNTEYBEAQDAIVKEIYNISSGYVPEMOTL 595
QY 593 AGVLAELDVLISFADLAASCTPTTRNISPDPDGDILLEGCRHPCVCAEADWNSIPND 652
Db 596 NDVLAQLDAVVSFAHVSNGAPVVRPALEKGGQRIILKASRHACVQDEIAFINDV 655
QY 653 RLVRGSENFQIITGNNGKSTYIRQGVNVLMAQVGSFVPCDNATISIRDCIFARVAG 712
Db 656 YFEKDKMFHITGNMGKSTYIRQGVNVLMAQVGSFVPCDNATISIRDCIFARVAG 715
QY 713 DCQLRGVSTFMEMLTASILKQATDRLSLIILDELGRSTYDGFGLAWALCEHIVEIK 772
Db 716 DSQKGVSTFMEMLTASILKQATDRLSLIILDELGRSTYDGFGLAWALCEHIVEIK 775
QY 773 APTLFATHFELTALANKGNGHKKAGIANGFVFAHIDPSNRKILMYKVPFGACDQS 832
Db 776 AFCHFATHFELTALANKGNGHKKAGIANGFVFAHIDPSNRKILMYKVPFGACDQS 825
QY 833 FGIHVAEPANPPSVVALAREKASELEDFSPATIPN-DIKEASKR---KREFDRHDVS 888
Db 826 FGIHVAELANFPKHFIECAKQALEBFBQVIGBSQGYDIMEPAKCKYLERE----- 878

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593	QY	ACVLAELDVLLSFADLAASCPTPYTRRNII	SPPTGDIILLEGCHPCVFAHDVNWISPNDC	652
596	Db	NDVLAQLDAVVVSFAHVNGSAEVPVRAIL	EKGQGRILIKASHACVRYQDSIAFIPNDV	655
653	QY	RLVRGESFQIITGPNMGKSTYIRQVGVNVL	MAQVGSFVPCDNATISIRDCIFARVGAG	712
656	Db	YFEKDQNFHIIITGPNMGKSTYIRQGVIVL	MAQICFPVPCESAESVIVDCILARVGAG	715
713	QY	DCOLRGVSTFQWCEMLTETASILKGATDR	SLIILDELGRGTSYDQFGLAWAI	CEHIVERIK 772
716	Db	DSQLKGVSTFMAEMLTETASILRSATKDS	LIILDELGRGTSYDQFGLAWAI	SEYIATKIG 775
773	QY	APTLPATFHIELTALANKGDNCHKQAGIAN	EHFVFAHIDPNSNRKILTMLYIKVHPGACDQ	832
776	Db	APCFMPATFHIELTALAN-----	QIPTVNNLHVTL--TTEETLTMLYQVKKGVC	825
833	QY	FGIHVAEAFNPSPSVVALAREKASELEDF	SPIALPN-DIKEAASR---KFEFDHIDS	888
826	Db	FGIHVAELANFPKHVIECAQKALEBEFQV	IGESQGYIMEPAKKCYLDERE-----	878
889	QY	RGTRAROFLODFAQLPDKMDPNVVRQKLS	KMKTDL	925
879	Db	OGEKIIIOEFLSVKOMPTEEMSEENITIKL	KOLKAEV	915

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RESULT 15
US-10-348-074-7
; Sequence 7, Application US/10348074
; Publication No. US20030176386A1
; GENERAL INFORMATION:
; APPLICANT: Morphotek Inc.
; APPLICANT: Grasso, Luigi
; APPLICANT: Kline, J. Bradford
; APPLICANT: Nicolaides, Nicholas C.
; APPLICANT: Sassi, Philip M.
; TITLE OF INVENTION: Method for Generating Engineered Cells for Locus Specific Gene
; TITLE OF INVENTION: Regulation and Analysis
; FILE REFERENCES: MG0003 US (MOR-0140)
; CURRENT APPLICATION NUMBER: US/10/348, 074
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/349,565
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 7
; LENGTH: 934
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-348-074-7

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Query Match	37.9%;	Score	1841.5;	DB	14;	Length	934;
Best Local Similarity	43.0%;	Pred. No.	3.6e-149;				
Matches	403;	Conservative	172;	Mismatches	307;	Indels	55;
Gaps	19;						
QY	14	LKLDAKQAQGLSFFKTLKDPD	-RAVLFRRDRDYTSHGDDATFI	ETVYHTTALRQLG	72		
Db	9	LQLESAAEVGFRRFQGMPEKPTT	TVLFDRGDFYTAHGEDALLAAREVFKTQGV	KYMG	68		
QY	73	NR-ADALSSVSVSRNMEETIARD	ILLBERMDLTLEYSGSN	-----WFLVKSGT	PGN	124	
Db	69	PAGAKNIQSIVLSSQNFESFVKD	ILLVROYR-VEVYKNRAGNKASKENDW	LYAYKASFGN	127		
QY	125	LGSPEDILFANNEMONGSPVIAAL	APNGQCEVGLGYVDITRKVLGLTEFLDDSH	TNL	184		
Db	128	LSQPEDILFGNNDMSASIGVGVK	MSAVDQGRQVGVGYVDSIQRLGLCEFPD	NDQFSNL	187		
QY	185	ESALVALGRCRECLVP-AET-GKS	SEYRPMFDAISRCGVVWYTERKKTBFK	GRDLVDQLRL	242		
Db	188	EALLIQIGKECVLPGETAGDMK	GLRQI---IQGGILITERKAFSTKDIYQD	LNRL	244		
QY	243	VKG-----SVBPVRDLVSGFEC	AGALGCILSYAELLADESNYGNVTKQYN	LSYM	294		
Db	245	LKGKKGOMNSAVLPEN-----	NOVAVSSLSAVTKFLELLSDSNFGOFEL	TTFDSQYM	300		

```

295 QY RLD$AAM$AL$N$M$E--$K$S$D$A$N$K$P$S$F$G$L$M$N$R$T$C$T$A$G$M$K$R$L$L$H$M$M$L$K$O$P$L$L$D$V$E$I$N$C$R 353
301 Db KLD$T$A$V$F$A$L$N$L$F$O$G$S$V$E$D$T$T$G$S$Q$S$L$A$L$N$K--$K$T$P$Q$Q$R$L$N$Q$W$I$K$O$P$L$M$D$K$N$R$I$E$R 359
354 QY L$D$L$Q$S$F$V$E$D$A$L$Q$D$L$R$Q$H--$L$K$H$I$D$P$I$E$R$L$T$H$L$N$E$R$K$R$A$S$I$V$H$V$K$L$Y$Q$S$T$R$V$P$Y$K$S 412
360 Db L$N$L$V$E$F$V$E$D$A$L$R$Q$T$Q$E$D$L$L$R$F$P$D$L$N$E$R$A$K$K$F$O$Q$A$N$L$Q$C$V$R$L$Y$Q$G$I$N$Q$L$N$V$T$Q 419
413 QY V$L$E$R$D$G$O$F$A$L$I$R$E$R$Y$D$S$L$E$K$W$S$D$D$N$H$L$N$K$I$G$L$V$E$T$S$V$D$L$Q$J$E$N$G$E$Y$M$I$S$S$A$Y$D$N 472
420 Db A$L$E$K$H$E$G$K$H$Q$K$L$L$A$V$F$T$P$L$T$D$L$R$D--$F$S$K$Q$E$M$I$E$T$T$L$D$M$D$Q$E$N$H$E$F$L$V$K$P$S$F$D$N 477
473 QY L$S$A$L$K$D$E$O$E$T$E$R$Q$I$H$N$L$H$Q$T$A$N$D$L$D$L$P$L$D$K$S$L$K$D$K$E$T$Q$F$G$H$V$P$R$I$T$K$E$E$P$K$V$K$Q$L 532
478 Db L$S$E$L$E$I$M$N$D$L$E$K$Q$M$Q$S$T$L$S$A$A$R$D$L$G$D$P$G$K$I$D$S$S$A$Q$F$G$Y$Y$F$R$V$T$C$K$E$E$K$V$L$R$N-- 535
533 QY N$S$H$Y$T$V$L$E$T$R$D$G$V$K$F$T$V$T$K$L$G$L$D$G$F$Q$K$I$V$E$Y$K$S$C$Q$K$E$L$V$A$R$V$V$Q$T$A$A$S$F$S$E$V$F$A$G 592
536 Db N$K$N$F$T$V$D$I$Q$K$G$V$K$F$N$S$K$L$T$S$N$E$Y$T$K$N$K$Y$E$B$A$Q$D$A$I$V$K$E$I$V$N$T$S$S$G$V$E$P$M$Q$L 595
593 QY A$G$V$T$A$E$L$D$V$L$S$P$A$L$A$A$S$C$P$T$Y$R$P$N$I$S$P$D$T$G$D$I$I$E$G$C$H$P$C$V$E$A$Q$D$W$N$S$I$P$N$D$C 652
596 Db N$D$V$L$A$Q$L$D$A$V$S$F$A$H$S$N$G$A$P$V$P$V$R$A$I$L$E$K$G$Q$R$I$L$K$S$H$A$C$V$E$Q$D$E$I$A$F$I$P$N$D$V 655
653 QY K$L$V$R$E$S$F$Q$I$T$G$N$M$G$K$S$T$Y$I$Q$Y$G$V$N$V$L$A$Q$V$S$F$V$P$C$N$A$T$I$S$I$R$D$C$I$F$A$R$V$G$A 712
656 Db Y$E$K$D$K$O$M$F$H$I$T$G$N$M$G$K$S$T$Y$I$Q$Y$G$V$L$V$L$A$Q$Y$G$C$F$V$P$C$S$A$R$S$I$V$D$C$I$A$R$V$G$A 715
713 QY D$Q$L$R$G$V$T$F$Q$E$M$L$E$T$A$S$I$L$K$G$A$T$D$R$S$L$I$I$D$E$L$G$R$T$Y$D$G$F$G$L$A$W$A$I$C$E$H$I$V$E$E$I$K 772
716 Db D$Q$L$K$G$V$T$F$W$A$E$L$E$T$A$S$I$L$R$S$A$T$K$D$S$L$I$I$D$E$L$G$R$T$Y$D$G$F$G$L$A$W$A$I$S$E$Y$I$A$T$K$I$G 775
773 QY A$P$T$L$P$A$T$H$E$L$T$A$L$A$N$K$G$N$G$H$K$Q$N$A$G$I$A$N$H$V$F$A$H$I$D$P$S$N$R$K$I$T$M$L$Y$K$V$H$P$G$A$C$D$S 832
776 Db A$F$C$M$P$A$T$H$E$L$T$A$L$N-----Q$I$P$T$V$N$N$L$E$V$T$A$L--$T$T$E$T$I$T$M$L$Y$Q$V$K$K$G$V$C$D$S 825
833 QY F$G$I$H$V$A$E$A$N$P$P$S$V$A$L$A$R$E$K$A$S$E$L$D$E$S$P$A$I$P$N--D$I$K$E$A$S$K$R--$K$R$E$D$R$H$D$V 888
826 Db F$G$I$H$V$A$E$L$A$N$P$K$H$V$E$C$A$Q$K$A$E$L$E$F$O$Y$I$G$E$S$Q$G$Y$I$M$E$P$A$N$K$C$Y$L$E$R----- 878
889 QY R$G$T$A$R$A$F$O$Q$F$A$Q$L$P$L$D$K$M$D$P$N$V$V$R$Q$K$L$S$K$M$K$D$L 925
879 Db O$E$K$T$I$O$E$F$I$S$K$V$K$O$M$P$T$E$S$E$N$T$I$T$K$L$K$O$L$K$A$E$V 915

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Search completed: April 7, 2004, 10:52:31
Job time : 56 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 9, 2004, 05:00:27 ; Search time 205 Seconds
(without alignments)
8210.566 Million cell updates/sec

Title: US-10-029-065-1

Perfect score: 3033

Sequence: 1 ataaaggttaagaaaaa.....tatcttatatggtcaaaaa 3033

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 692709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

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2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	420.8	13.9	2805	4	US-09-651-656-4
2	420.8	13.9	2805	4	US-09-650-855-4
3	420.8	13.9	2947	1	US-08-457-176-1
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5	420.8	13.9	2947	4	US-09-220-132-8
6	420.8	13.9	3145	4	US-09-708-200-14
7	420.8	13.9	3145	4	US-09-708-200-14
8	335	11.0	3823	4	US-09-512-250C-1
9	234	7.7	723	4	US-09-651-656-2
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13	135.8	4.5	3754	3	US-08-526-840B-31
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17	127	4.2	2676	4	US-09-134-001C-2076
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20	122.2	4.0	2658	4	US-09-489-039A-2980
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25	120.6	4.0	2568	2	US-08-468-558-1
26	120.6	4.0	2568	3	US-08-676-444-1
27	106	3.5	3093	2	US-08-588-521-7

ALIGNMENTS

RESULT 1

US-09-651-656-4

; Sequence 4, Application US/09651656

; Patent No. 6340566

; GENERAL INFORMATION:

; APPLICANT: MCCUTHEN-MALONEY, SANDRA

; TITLE OF INVENTION: DETECTION AND QUANTITATION OF SINGLE NUCLEOTIDE

; TITLE OF INVENTION: POLYMORPHISMS, DNA SEQUENCE VARIATIONS, DNA MUTATIONS,

; FILE REFERENCE: IL-10699

; CURRENT APPLICATION NUMBER: US/09/651,656

; PRIOR FILING DATE: 2000-08-29

; PRIOR APPLICATION NUMBER: 60/192,764

; NUMBER OF SEQ ID NOS: 106

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 4

; LENGTH: 2805

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-651-656-4

Query Match	13.9%	Score	420.8	DB	4	Length	2805
Best Local Similarity	51.3%	Pred. No.	6.4e-117				
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Db	407	TGCTAATAATGAATGCAAAATCTCCGGTGATGCTGTCTTGTGCTTCCAAACATTCGGTC	466				
Qy	479	AGAT	538				
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Qy	539	CAGAAATTCCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	598				
Db	527	GTGAATTCCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	586				
Qy	599	GCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	658				
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Qy	659	ATGCAATATCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	718				
Db	644	AGATAATTCAGAGAGGAGGAATTCATGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	703				

Sequence 4, Appli
Sequence 4, Appli
Sequence 4555, Ap
Sequence 4296, Ap
Sequence 16, Appl
Sequence 16, Appl
Sequence 3080, Ap
Sequence 53, Appl
Sequence 30, Appl
Sequence 1, Appl
Sequence 907, App
Sequence 37, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 2813, Ap
Sequence 332, App
Sequence 14, Appl

; CURRENT FILING DATE: 2000-08-29
 ; PRIOR APPLICATION NUMBER: 60/192,764
 ; PRIOR FILING DATE: 2000-03-28
 ; NUMBER OF SEQ ID NOS: 106
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 2805
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-650-855-4

Query Match 13.9%; Score 420.8; DB 4; Length 2805;
 Best Local Similarity 51.3%; Pred. No. 6.4e-117;
 Matches 1194; Conservative 0; Mismatches 1072; Indels 60; Gaps 7;
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 Qy |||||
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 Db |||||
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 Qy |||||
 719 GAGATTGGTACAGGATCTTGGTAGGCTCTCAAGGTTCA-----GTAGAAC 766
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 2192 AAATGCTTCTATCTCAGGCTCTGCAACCAAGATTCATTAATCATAGATGAATGG 2251
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RESULT 3

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US-08-457-176-1
; Sequence 1, Application US/08457176
; Patent No. 5591826
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: de la Chappelle, Albert
; TITLE OF INVENTION: Mutator Gene and Hereditary
; TITLE OF INVENTION: No. 5591826-Polyposis Colorectal Cancer
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie, and Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,176
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160295
; FILING DATE: 02-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.44900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202.508.9100
; TELEFAX: 202.508.9299
; TELEX: 197430 BEMB UT
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2947 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

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; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-457-176-1

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Query Match 13.9%; Score 420.8; DB 1; Length 2947;
Best Local Similarity 51.3%; Pred. No. 6.6e-117;
Matches 1194; Conservative 0; Mismatches 1072; Indels 60; Gaps 7;

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 Db 2020 TTCTAATGAGTATCTTTGAAAGAAATACAGATGTTCCACATCATCTACTGCCCCA 2079
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 Db 2080 ATATGGGAGGTAAATCAACATATATTCACAAACTGGGGTGATAGTACTCATGCCCCAA 2139
 Qy 2084 TTGGCTGTTTGTCCATGTGACATGCTACCATTTCTATTCGTGATGTATTTTGTCTC 2143
 Db 2140 TTGGGTGTTTGTGCCATGAGTCAGCAGTCAATTAAGAGAGTCTCCAGTTTATGCTGATGCCC 2199
 Qy 2144 GTGTGGCGCTGGAGATTCAGCAGTGGAGAGGTTTCTACTTTTATGCAAGAGATGCTTG 2203
 Db 2200 GAGTAGGGCTGGTGGAGAGTCAATTAAGAGAGTCTCCAGTTTATGCTGAAATGTTGG 2259
 Qy 2204 AGATCGATCGATCTTGAAGAGGCTACTGATGATCATTTGATTAATTAATGATGAGTTGG 2263
 Db 2260 AAACTGCTTCTCTCTCAGGTCTGCAACCAAGATTCATTAATAATCATAGATGAATGG 2319
 Qy 2264 GCGTGGGACATCACTTACGATGCTTTGTTAGCTTGGCTATTTGTGAGCAGATTTG 2323
 Db 2320 GAAGAGGAATCTTACCTTACGATGATTTGGTTAGCATGGGCTATATCAGAAATACATTG 2379
 Qy 2324 TTGAAGAAATTAAGCACCACATTTGTTGCACTTCTCATGAGTCACTGCTCATTTAG 2383
 Db 2380 CAACAAGATTTGGTGTCTTTTTCATGTTTGAACCAATTTTCATGAACTTACTGCTTGG 2439
 Qy 2384 CCAACAGATGGAGCAATGGACATAAGAAATGCTGGGATAGCAAAATTTTCATGTTT 2443

Db 2440 CCATCAG-----ATACCACTGTTAAATCTCATGTCA 2475
 Qy 2444 TTGCACATGACCCCTTCTAATGCGAAGCTAATCTGCTTTTACAGGTTTCCACAGGTG 2503
 Db 2476 CAGCACTCA-----CCACTGAAGAGACCTTAACTATGCTTTTATCAGGTGAAGAAAGTG 2529
 Qy 2504 CTTGTGATCAGATTTTGGTATTTCATGCTGCTGAATTTGCAAAATTTTCCACCGAGTTG 2563
 Db 2530 TCTGTGATCAAAAGTTTGGGATTCATGTTGAGAGCTTGTCTAATTTCCCTAAGCATGTAA 2589
 Qy 2564 TGGCTCTGGCTAGAGAAAGGCATCTCAGTTGGAGGATTTCTCTCTTATTGGCCATAATTC 2623
 Db 2590 TAGAGTGTCTAAACAGAAAGCCCTGGAACCTTGAGGAGTTTTCAGTATATTGGAGATGCG 2649
 Qy 2624 CAATGACATTAAGAGCGAGCTTCAAAACGGAAGAGAGAAATTTGA 2669
 Db 2650 AAGGATATGATATCATGTGAACCAAGCAGCAGCAAAAGAGTGTCTATCTGGA 2695

RESULT 4

US-08-457-175-1
 ; Sequence 1, Application US/08457175
 ; Patent No. 5693470
 ; GENERAL INFORMATION:
 ; APPLICANT: Vogelstein, Bert
 ; APPLICANT: Kinzler, Kenneth W.
 ; APPLICANT: de la Chappelle, Albert
 ; TITLE OF INVENTION: Mutator Gene and Hereditary
 ; TITLE OF INVENTION: No. 5693470-Polypsis Colorectal Cancer
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Banner, Birch, McKie, and Beckett
 ; STREET: 1001 G Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20001
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/457,175
 ; FILING DATE: 01-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/160295
 ; FILING DATE: 02-DEC-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kagan, Sarah A.
 ; REGISTRATION NUMBER: 32,141
 ; REFERENCE/DOCKET NUMBER: 01107.44900
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202.508.9100
 ; TELEFAX: 202.508.9299
 ; TELEX: 197430 BMB UT
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2947 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cdna
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens
 ; US-08-457-175-1

Query Match 13.9%; Score 420.8; DB 1; Length 2947;
 Best Local Similarity 51.3%; Pred. No. 6.6e-117;
 Matches 1194; Conservative 0; Mismatches 1072; Indels 60; Gaps 7;

QY 359 ACTGGAGACTGGTAAAGTGAACCCAGGAACTCTTGGAGTATTTTCAGGATATCTGT 418
Db 415 ATTGGTATTTGGCATAAAGCTTCTCTCGCAATCTCTCTCAGTTTGAAGACATCTCT 474
QY 419 TTGCTAATAATGAATGCAAAATTTCTCGGTGATTTGCTGCTCTTGGCTCCAACTTCGGTC 478
Db 475 TTGCTAACAATGATATGTACAGCTTCCATTTGCTGTTGGGTGTTTAAATGTCGCCAGTTG 534
QY 479 AGAATGATGTGAAGTTGGCTTAGCTATGTGTATATTAATAAGAGAGTCTTGGTTTAA 538
Db 535 ATGCCACAGACAGAGTTGGAGTTGGGTATGTGGAATCCATACAGAGGAAACTAGGACTGT 594
QY 539 CAGAAATTTCTAGATGATAGCCACTTCAAAATTTGGAGTCTGTTGGTCTCTTCTGTT 598
Db 595 GTGAATTTCCCTGATAATGATCAGTTCTTCAATCTTGGCTCTCTCATCAGATTTGAC 654
QY 599 GCAGAGAAATGCTTTGTACACGGGAGACTGCCAAATCCAGTGAATACAGGCTATGTTTG 658
Db 655 CAAAGGAATGTTTTACCCGGAG--GAGAGACTGCTGGAGACATGGGGAACCTGAGAC 711
QY 659 ATGCAATATCTAGATGGCGGTGATGTGTAATCTGAAGAAAGAAACTGAATTTAAAGGGA 718
Db 712 AGATAATTTCAAGAGGAGGAATCTGATCAAGAAAGAAAGAAAGCTGACTTTTCCCAA 771
QY 719 GAGATTTGGTACAGGATCTTGGTAGGCTCGTCAAGGGTTCA-----GTAGAAC 766
Db 772 AAGACATTTATCAGGACTCAACCGTGTGTTGAAGGCAAAAGGGAGAGACAGATGAATA 831
QY 767 CTGTTTCAGAAATTTGGTCTCTGGTTCGAAATGTGCATCAGGCGCTTTGGGGTGCATCTTT 826
Db 832 GTGCTGTATTGCCAGAAATGGAATCAGGTGCGAGTTTCATCACTGTCTCGCGTAAATCA 891
QY 827 CTTATGACAGACTTACTTCCGATGAGGACCACTATGGAATATACAGTCAAAATACA 886
Db 892 AGTTTGTAGAACTCTTATCAGATGATTTCCAACTTTGGACAGTTTGAACGTGACTACTTTG 951
QY 887 ACCTCAATAGTTATCAGATTTAGATTTCTGCTGTATGAGAGCACTGAATGTTATGAGA 946
Db 952 ACTTCAGCCAGTATATGAAATTTGATGATTTGAGAGCTTTTGTAGAATGCAATTTGAGG 1011
QY 947 GCAAAATCAGATGCTPAATAAAATTTTACGTTCTGATGAATAGAACGTTGACTG 1006
Db 1012 GTTCTGTTGAAGATACACCTGGCTCAGTCTCTGCTGCTGCTGCTGCTGAATGAAGTAA 1071
QY 1007 CTGGAATGGGTAAAGGTTATTTGACATGTTGGCTGAGCAACCTTTACTAGATCTAGAG 1066
Db 1072 CCCCTCAAGGACAAAGACTTTGTTAACCAAGTGGATTAAGCAGCCCTCTCATGATTAAGA 1131
QY 1067 AGATTAACCTGAGGCTGGATTTAGTTCAATCATTCGTGGAGGATGCTGGCTTCGCCAAG 1126
Db 1132 GAATAGAGGAGAGATTGAATTTAGTGGAGCTTTTGTAGAATGCAATTTGAGGCGAGA 1191
QY 1127 ATTTGAGGAGCAT---CTGAAAAGATTTTCAAGATTTGAGCGGCTGACACAACTCTTG 1183
Db 1192 CTTTACAGAAGATTTACTTCTGTCGATTTCCAGATCTTAAACCGACTTTCGCAAGAGTTTC 1251
QY 1184 AGAGGAAAGAGCCAGTTTACTGTCACGTTGTAAACCTATCATCTCAGTCAAGTACCAGGTAC 1243
Db 1252 AAAGACAGCAGCAACTTACAAGATTTGTTACCAGCTTATCAGGGTATAATCAACTAC 1311
QY 1244 CATATATCAAAAGTGTTTTGAAGCTCATGATGGCAATTTTGCACACTCATCAGGGAAA 1303
Db 1312 CTAATGTTTATACAGCTCTCGGAAAACATGAAGGAAACACACAGAAATTTATTTGGCAG 1371
QY 1304 GGTATATGATTTCTAGAGAAATGGAGTGTATGATATCACTGAATGAATTCATAGTGC 1363
Db 1372 TTTTGTGACTCTCTTACTGA-----TCTTCGTTCTGACTTCTCCAAAGTTTTCAGGAAA 1425
QY 1364 TTGTGGAACTTCTCTGACCTTGATCAACTTGTGAAATGGGAAATACATGATTTCTTCTG 1423
Db 1426 TGAAGAAACAACTTTAGATATGATCAGGTGGGAAACCACTGAATTCCTGTTAAACCTT 1485

QY 1424 CATATGATCCCAAAATTTATCTGCTCTGAAGGATGAGCAAGAGACATTTGAGCGCAAAATTC 1483
Db 1486 CATTTGATCTTAATCTCAGTGAATTTAGAGAAATATGAATGACTTGGAAAAGAGATGC 1545
QY 1484 ATAATTTGCACAAAACAACTGCCAATGATCTTGAATCTACCTATTTGATAAGTCACTTAAAC 1543
Db 1546 AGTCAACATTTAATAAGTGCAGCCAGAGATCTTGGCTGGACCCTGGCAACACAGATTTAAAC 1605
QY 1544 TAGATAAGAAAACACAAATTTGGGACAGCTCTTCAAGATTACCAAGAAAGAGAACCAAAAG 1603
Db 1606 TGGATTTCCAGTGCACAGTTTGGGATATTAATCTTCTGTAACTGTAAAGAAAGAAAAGTCC 1665
QY 1604 TCAGGAAGCAGCTAAATTTCTCACTCACTCTTCTCGAAAACACATGAAGATGGGGTAAAGT 1663
Db 1666 TTCTGTA-----CAATAAAACTTTAGTACTGTAGTATCCAGAGAAATGGTTHAAT 1719
QY 1664 TCACCTATACAAAACCTCAAAAACACTAGGAGATCAGTTTCCAGAGATTTGTAGAGAGTACA 1723
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QY 1724 AAGCTGTCAAGAAAGATTTGGTAGCTCGTGTAGTTCAAAACAGCTGCGAGTTTCTCCGAGG 1783
Db 1780 AAGAAGCCCGAGGATGCCATTTGTTAAAGAAATTTGCAATATTTCTTCAAGCTATGTAGAAC 1839
QY 1784 TGTTCGAGGTATAGCTGGTGTACTTTGCTCAGTTGGATGTGTACTCAGTTTTCGCGAAT 1843
Db 1840 CAATGCAGACACTCAATGATGTGTAGCTCAGCTAGATGCTGTGTGCTGCTTGTCTCAG 1899
QY 1844 TGGTGCAGTTGCCAACTCCCTTACACAAGACCAAAATATCATGTCACCCAGATACAGGAG 1903
Db 1900 TGTCAAAATGAGCAGCCCTGTTCCATATGTACGACAGCCATTTTGGAGAAAGGACAAGGAA 1959
QY 1904 ATATTATACTTGAAGGCTAGGATCCTCTGTGTGGAAGCTCAAGATTTGGTGAATTAACCTCA 1963
Db 1960 GAATTTATTTAAAGCAATCCAGGATGCTGTGTGGAAGTTCAAGATGAATTTGCAATTTA 2019
QY 1964 TTCTTAATGACTGTAGACTAGTTAGGGGAGAGAGTTTGGTTTTCAGATTTATCACAGGCCCTA 2023
Db 2020 TTCTTAATGACGTATATCTTTGAAAAGATATAACAGATGTTCCACATCATTTACTGGCCCCA 2079
QY 2024 ACATGGGTGAAAAGTGCACCTACATTCGCGAGGTGGTGTGAATGTCCTGATGCGCCCAAG 2083
Db 2080 ATATGGGAGGTAAATCAACATATATTCGACAACTGGGGTGTAGTACTCATGCGCCCAAA 2139
QY 2084 TTGCTGCTTTTGTTCATGTGACAAATGCTACCAATTTCTATTCGTGATGTTATTTTGTCTC 2143
Db 2140 TTGGGTGTTTTGTGCCATGTGAGTCAGCAGAAAGTGTCCATTTGGACTGTCATCTTAGCCC 2199
QY 2144 GTGTTGGCGCTGGAGATTTGCCAGCTGAGAGAGTTTCTACTTTTATGCAAGAGATGCTTG 2203
Db 2200 GAGTAGGGGCTGGTGACAGTCAATTTGAAAGGAGTCTCCAGTTTCATGGCTGAAATGTTGG 2259
QY 2204 AGACTGCATCGATCTTGAAGGAGCTACTGATAGATCATTTGATTAATTTGATGAGTTGG 2263
Db 2260 AAATCTGCTTCTATCTCTCAGGTCTGCAACCAAGATTCATTAATAATCATAGATGAATGG 2319
QY 2264 GCGTGGGACATCAACTACAGTGGCTTTGTTTGTAGCTTGGGCTATTTTGTGAGCACATTG 2323
Db 2320 GAAGAGGAATCTTACCTCAGATGGATTTGGTTAGCATGGGCTATATCAGATACATTG 2379
QY 2324 TTGAAGAAATTAAGACCAACCAATTTTGGCCACTCATCTTTCATGAGCTGACTGCAATTAG 2383
Db 2380 CAACAAGATTTGGTGTCTTTTGTGATGTTTGCACCCCACTTTTTCATGAACCTTACTGCCTGG 2439
QY 2384 CCAACAGAAATGGAGCAATGGACATAAGAAAATGCTGGGATAGCAAAATTTTCATGTTT 2443
Db 2440 CCAATCAG-----ATACCAACTGTTAATAATCTCATGTCA 2475
QY 2444 TTGCACACATTTGACCTTCTAATTCGCAAGCTAATACTGCTTTTCAAGGTTTCAACCCAGTG 2503
Db 2476 CAGACTCA-----CCACTGAAAGAGACCTTAATGCTTTATCAGGTGAAGAAAGGTG 2529
QY 2504 CTTGTGATCAGAGTTTGGTATTTCATGTTGCTGAAATTTTGCAAAATTTTCCACCGAGTGTG 2563

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Db 2530 TCCTGATCAAGATTGTTGGGATTCATGTTGAGAGCTTGCTAATTTCCCTAAGCATGTAA 2589
QY 2564 TGGCTCTGGCTAGAGAAAGCATCTGAGTTGGAGGATTTCTCTCCATTATGCCAATAATTC 2623
Db 2590 TAGAGTGTGCTAAACAGAAAGCCCTGGAACTTGAGGAGTTTCAGTATATTGGGAATCGC 2649
QY 2624 CAAATGACATTAAAGAGCGCTTCAAAACGGAGAGAGATTGA 2669
Db 2650 AAGATATGATATCATGAAACCGAGCAGCAAAAGAGTGTCTATCTGGA 2695

RESULT 5
US-09-220-132-8
; Sequence 8, Application US/09220132
; Patent No. 650607
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
; OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 07334-074001
; CURRENT APPLICATION NUMBER: US/09/220,132
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: US 60/068,821
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 2947
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-220-132-8

Query Match 13.9%; Score 420.8; DB 4; Length 2947;
Best Local Similarity 51.3%; Pred. No. 6.6e-117;
Matches 1194; Conservative 0; Mismatches 1072; Indels 60; Gaps 7;

QY 359 ACTGGGAGACTGGTAAAGTGGAAACCCAGGGAATCTTGGAAAGTTTGGAGATATTCCTGT 418
Db 415 ATTGGGATTTGGCATATAGGGCTTCTCTCGCAATCTCTCTCAGTTTGAAGACATTCCTCT 474
QY 419 TTGCTAATATGAATCAAAATTCCTCGGTGATGCTGCTCTTGTCCAACTTCGGTC 478
Db 475 TTGGTACATATGATGTACGTTCCATCTGCTGTTGGGTGTTAAATGTCGCGAGTTG 534
QY 479 AGAATGGATGTGAAGTTGGCTTAGGCTATGTTGATATTAAGAGAGAGTCTCTTGGTTAA 538
Db 535 ATGCCCAGAGACAGGTTGGAGTTGGGTATGTTGATTCATACAGAGGAACTAGGACTGT 594
QY 539 CAGAAATTTAGATGATAGCATTCAAAATTTGGAGTCTGCTTGGTTGCTCTTGGTT 598
Db 595 GTGAATTTCCCTGATAATGATCAGTTTCCCAATCTTGAGGCTCTCTCATCCAGATTGGAC 654
QY 599 GCAGAGATCTCTTTGACAGCGGAGACTGCGCAATCCAGTGAATACAGGCTATGTTG 658
Db 655 CAAAGGAATGTGTTTACCGGAG---GAGAGACTGCTGGAGACTGGGGAACCTGAGAC 711
QY 659 ATGCAATATCTAGATCGCGGTGATGTGTAATCAAGAAAGAAAGAACTGAATTTAAAGGGA 718
Db 712 AGATAATTTCAAGAGGAGGAATTTCTGATCAGAAAGAAAGAAAGCTGACTTTTCCACAA 771
QY 719 GAGATTGGTACAGGATCTTGGTAGGCTCTCAAGGTTCA-----GTAGAAC 766
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QY 767 CTGTTTCAGATTTTGGTCTCTCGGTTCCGAATGTGATCAGCGGCTTTGGGGTGCATCTTT 826
Db 832 GTGCTGTATTGCCAGAANTGGAGATCAGGTTGCGAGTTTCATCAGTCTCTGCGGGTAATCA 891
QY 827 CTTATGCAAGAACTACTTGGCGATGAGCAACTATGGAAGTATACAGTCAAAACAATACA 886

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Db 892 AGTTTTAGAACTCTTATCAGATGATTCCAACTTTGGACAGTTTGAAGTACTGACTACTTTG 951
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QY 1067 AGATTAACTGTAGCTGGATTATAGTTCAATCATTTGPGGAGGATGCTGCGCTTCGCAAG 1126
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QY 1184 AGAGGAAAGAGCCAGTTTATGTCACGTTTGTAAACTCTATCACTCAAGTACCAGACTAC 1243
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Db 1312 CTAATGTTATACAGGCTCTGGAAAAACATGAGGAAAAACACCAGAAATTTATGTTGGCAG 1371
QY 1304 GGTATATTGATTCTCTAGAGAAATGGAGTATGATCAATCACTCAAGTAAAGTTCATAGTC 1363
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QY 1364 TTGTGAAACTTCTGTGACTTTGATCAACTGAGAAATGGAGAAATACATGATTTCTTCTG 1423
Db 1426 TGATAGAAACAACTTTAGATATGATCAGGTGAAACCACTGAATTCCTTTGTAACCTT 1485
QY 1424 CATATGACCAAAATTTATCTGCTCTGAAGATGAGCAGAGACATTTGGAGCGGCAAAATTC 1483
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QY 1544 TAGATAAGAGAAACACAAATTTGGACAGCTCTTCAAGAAATTAACAAAGAAAGAACCAAAAG 1603
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QY 1604 TCAGGAGCAGCTAAATTTCTACTACATGTTTCTCGAAACACATAGGATGGGTTAAAGT 1663
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QY 1784 TGTTCAGGATAGCTGCTGCTACTTGTGAGTTGGATGTTTACTGAGTTTGGCGGAT 1843
Db 1840 CAATGAGACACTCAATGATGTTTAGCTCAGCTAGATGCTGTTGTCAGCTTGTCTCAG 1899
QY 1844 TGGCTGCCAGTTGGCCAACTCCCTACACAAAGCAAAATATCAGTCCACAGATACAGGAG 1903
Db 1900 TGTCAATGAGCACTGTTTCCATATGTAGACACAGCCATTTTGGAGAAAGGACAGGAA 1959
QY 1904 AVATTATACCTTGAAGGGTGTAGGATCTCTTGTGTGAAGCTCAAGATTTGGGTTAACTCCA 1963
Db 1960 GAATTATATTAAAGCATCCAGGCTGCTTGTGTTGAAGTTCAAGATGAAATTTGCATTTA 2019

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1424 CATATGACCCAAATTTATCTGCTCTGAAGATGAGCAAGAGACATTTGGACGACAAATTC 1483
 1486 CATTTGATCTTAATCTCAGTGAATTAAGAAATAATGAATGACTTTGGAAAGAGATGC 1545
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 1666 TTCGTA-----CAATAAAACCTTAGTACTGTAGATATCCAGAGAAATGGGTAAAT 1719
 1664 TCACCTATACAAACTCAAAACACTAGGAGATCAGTTTCCAGAAATTTGTAGAGAGTACA 1723
 1720 TTACCAACAGCAATTTGACTTCTTTAAATGAAGATATACCAAAATAAAACAGAAATATG 1779
 1724 AAGCTGTGAGAAAGATTTGGTAGCTGTGTAGTTTCAACAGCTGCGAGTTTCCGAGG 1783
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 1784 TGTTCGAGGTATAGCTGGTGTACTTGTCTGAGTTGGATGTTACTGAGTTTTCGGAAT 1843
 1840 CAATGACAGACTCAATGATGTTGTAGTCTGAGTATGATGCTGTGTCAGCTTTGCTCAG 1899
 1844 TGGCTGCCAGTTGCCAACTCCCTACACAGACCAAAATATCATGTCACCAAGATACAGGAG 1903
 1900 TGTCAAAATGAGCAGCTGTTCCTATATGTACGACGACCAATTTTGGAGAAAGCAAGGAA 1959
 1904 ATATTATCTTGAAGGTGTAGGATCTTGTGTGGAAGCTCAAGATGGGTAACTCCA 1963
 1960 GAATTAATTAAGAGCATCCAGGATGCTGTGTGAAGTTCAAGATGAATTTGCAATTA 2019
 1964 TTCTTAATGACTGTAGACTAGTTTGGGGAGAGAGTTGTTTTCAGATTTATCACAGGCCCTA 2023
 2020 TTCTTAATGACTGTATCTTTGAAAAGATTAACAGATTTTCCATCATTTACTGGCCCA 2079
 2024 ACATGGTGAAGTGCAGCTCATTTCCGAGGTTGGTGTGAATGCTCTGATGGCCCAAG 2083
 2080 ATATGGAGGTAAATCAACATATTTTCAAACTGGGGTGAAGTACTCATGGCCCAAA 2139
 2084 TTGGCTCGTTTGTTCATGTGCAATGCTTACCAATTTCTATTGTGATTTGTTGCTC 2143
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 2200 GAGTAGGGCTGGTGACAGTCAATTTGAAGAGTCTTCCAGTTCATGGCTGAAATGTTGG 2259
 2204 AGACTGCATGGAATTTGAAGAGGACTTCTGATAGATCATGTATTAATGATGAGTTGG 2263
 2260 AACTGCTTCTATCTTCCCTCAGGCTGCAACCAAGAAATTTCAATAATCATAGATGAATGG 2319
 2264 GCGTGGGACATCAACTAGAGGCTTTGGTTTGTAGCTTTGGGCTATTTGTGAGCAATTTG 2323
 2320 GAAGAGAACTTCTACTCAGATGGAATTTGGGTTAGCATGGGCTATATCAGAAATATG 2379
 2324 TTGAAGAAATTAAGCAACCAATTTTGGCCACTCCTTTCATGAGTGCATGCAATTAG 2383
 2380 CAACAAGATTTGCTGCTTTTGTGATGTTTGCACACCAATTTTCAATGACTTCTGCTGG 2439
 2384 CCAACAGAAATGGAGCAATGGACATAGAAAATGCTGGGATGAGCAATTTTCATGTTT 2443
 2440 CCAATCAG-----ATACCACTGTTAATAATCTACATGTCA 2475
 2444 TTGCACATTTGACCTTTCTAATCGCAAGCTTAATGCTTATGCTTTTCAAGAGTTTCCACGGTG 2503
 2476 CAGCACTCA-----CCACTGAAGAGACCTTAACTATGCTTTTATCAGTGAAGAAAGGTG 2529

2504 CTTGTGATCAGAGATTTTGGTATTCTATGTTGCTGAATTTGCAAAATTTCCACCGAGTGTG 2563
 2530 TCTGTGATCAAGATTTTGGGATTTCAATTTGCAAGAGCTTGTCTAATTTCCCTAAGCAATGAA 2589
 2564 TGGCTCTGGCTAGAGAAAAGGCAATCTGAGTTGGAGGATTTCTCTCTTATTTGCCATATTC 2623
 2590 TAGAGTGTCTAAACAGAAAGCCCTGGAACCTTGGAGGTTTCAGATATATTGGAGATCGC 2649
 2624 CAAATGACATTTAAAGAGGCGAGCTTCAAAACGGAAGAGAGAAATTTGA 2669
 2650 AAGGATATGATATCATGGAACCAAGCAGCAAGAAAGTGTCTATCTGGA 2695

RESULT 7
 US-09-788-657-9
 ; Sequence 9, Application US/09788657
 ; Patent No. 6656736
 ; GENERAL INFORMATION:
 ; APPLICANT: Nicolaides, Nicholas
 ; APPLICANT: Sasse, Philip
 ; APPLICANT: Kinzier, Kenneth
 ; APPLICANT: Grasso, Luigi
 ; APPLICANT: Vogelstein, Bert
 ; TITLE OF INVENTION: Methods for generating hypermutable
 ; FILE REFERENCE: 01107.00097
 ; CURRENT APPLICATION NUMBER: US/09/788,657
 ; CURRENT FILING DATE: 2001-02-21
 ; PRIOR APPLICATION NUMBER: 60/184,336
 ; PRIOR FILING DATE: 2000-02-23
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 9
 ; LENGTH: 3145
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-788-657-9

Query Match 13.9%; Score 420.8; DB 4; Length 3145;
 Best Local Similarity 51.3%; Pred. No. 6.9e-117;
 Matches 1194; Conservative 0; Mismatches 1072; Indels 60; Gaps 7;

359 ACTGGAGACTGTATAAAGTGGAAACCCAGAGGAATCTTGGAGTTTGGAGTATTTCTGT 418
 415 ATTGGTATTGGCATATAGAGCTTCTCTGGCAATCTCTCAGTTTGAAGACATTTCTCT 474
 419 TTGCTAATAATGAAATGCAAAATTTCTCCGGTGATTTGCTGCTCTTGTCTCCAAATCTCGGTC 478
 475 TTGGTAAACATGATATGTCAGCTTCCATTTGGTGTGTGGGTGTTAAATGTCGCGAGTTG 534
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 535 ATGGCCAGAGACAGGTTGGAGTTGGGTATGTGGATTTCCATACAGAGGAACTAGGACTGT 594
 539 CAGAAATTTCTAGATGATAGCCACTTCAAAATTTGGAGTCTGCTTTGGTGTCTCTTGGTT 598
 595 GTGAATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 654
 599 GCAGAGAAATGCTTTGTACCCAGCGAGACTGGCAAAATCCAGTGAATACAGGCTATGTTTG 658
 655 CAAAGAAATGTTTATCCCGAG--GAGAGACTGCTGGAGACATGGGAAACTGAGAC 711
 659 ATGCAATATCTAGATGCGCGCTGATGGTAACTGAAGAAAGAAAGAACTGAATTTAAAGGA 718
 712 AGATAATTTCAAAGAGAGGAAATTTCTGATCACAAGAAAGAAAGAAAGCTGACTTTTCCACA 771
 719 GAGATTGGTACAGGATCTTGGTAGGCTCTGCAAGGGTTCA-----GTAGAAC 766
 772 AAGACATTTATCAGGACCTCAACCGGTTGTTGAAGGCAAAAGGAGAGAGAGATGAATA 831
 767 CTGTTTCGAGATTTGCTCTCTGGGTTTCAATGTCATCAGGCGCTTTGGGGTGCATCTTT 826
 832 GTGCTGTATTGCCAGAAATGGAGATCAGGTTGCGAGTTTCATCTGCTGCGGTAAATCA 891

QY 827 CTTATGACAGACTTTCGGATGAGCAACTATGAACTATACAGTCAACAACTACA 886
 Db 892 AGTTTGTAGAACTCTTATCAGATGATTCACAACTTTGCAAGTTTGAAGTCTACTTTTG 951
 QY 887 ACCTCAATAGTTATCATGAGATTAGATTCTGCTCTATGAGAGCACTGAATGTTATGAGA 946
 Db 952 ACTTCAGCCAGTATGAAATTTGATATTCAGCAGTTCAGAGCCCTTAACCTTTTTCAGG 1011
 QY 947 GCAATCAGATGCTAATAAATTTTACGTTTGTGTTTGGTCTGATGATAGAACGTTGACTG 1006
 Db 1012 GTTCTGTGTAAGATACCACTGGCTCTCAGTCTCTGGCTGCTCTTGTGAATAAGTGAATA 1071
 QY 1007 CTGGAATGGGTAAAGGTTATTCACATGTTGGCTGAAAGCAACCTTTACTAGATGTAGAAG 1066
 Db 1072 CCCTCAAGCAAGAACTTTGTTAAACAGTGGATTAAGCAGCTCTCATGATGAAGAAACA 1131
 QY 1067 AGATTAACTGTAGCTGGATTTAGTTTCAATCATTCGTGGAGGATGTCGCTTTGCGCAAG 1126
 Db 1132 GAATAGAGGAGAGATTGAATTTAGTGAAGCTTTTGTAGAAGATGCAAGATTGAGGCAGA 1191
 QY 1127 ATTTGAGGAGCAT---CTGAAGAATTTTACATATTGAGCGGCTGACACACATCTTG 1183
 Db 1192 CTTTACAGAAGATTTACTTCTGATTCCTGATTCCTGATCTTAACCGACTTGCACAGAGTTT 1251
 QY 1184 AGAGAAAGAGGCGAGTTTATGTCAGCTTGTAACTCTATCATCTCAAGTACCAGAGTAC 1243
 Db 1252 AAGACAGCAGCAAACTTACAGATTGTTTACCAGCTCTATCAGGGTATTAATCAACTAC 1311
 QY 1244 CATATATCAAAAGTGTGTTTGGAACTGATGATGGCAATTTGCAACACTCATCAGGAA 1303
 Db 1312 CTAATGTTATACAGCTCTCGAATAACATGAAGAAACACCAAGAAATTTTGTGGCAG 1371
 QY 1304 GGTATATTGATTCCTAGAGAAATGGAGTGTGATGATATCACTCAATGAATTTTATAGTTC 1363
 Db 1372 TTTTGTGACTCTCTTACTGA-----TCTGCTCTGACTTCTCAGGTTTCAGGAAA 1425
 QY 1364 TTGTGAAACTCTCTGTGACCTTGTATCAACTGAGAAATGAGAAATACATGATTTCTTCTG 1423
 Db 1426 TGATAGAAACAATTTAGATATGATCAGGTGGAACCATGATTTCTTGTAAACCTT 1485
 QY 1424 CATATGACCAAAATTTATCTGCTCTGAAAGATGAGCAAGAGACATGAGGCGCAAAATTC 1483
 Db 1486 CATTTGATCTTAATCTCAGTGAATTAAGAGAAATAATGAATGACTTGGAAAGAGATGC 1545
 QY 1484 ATRATTTGCAACAACAACTGCGCAATGATCTTGTATCTTACCTATTGATAAGTCACTTAAC 1543
 Db 1546 AGTCAACATTAATTAAGTGCAGCCAGAGATCTTGGCTTGGACCTTGGCAACAGATTAAAC 1605
 QY 1544 TAGATAAGAAACAATAATTTGGACACGCTCTTTCAGAAATTCACAAAGAAAGAACCAAAAG 1603
 Db 1606 TGGATTCAGTGCACAGTTTGGATATTACTTTTCTGTAACTGTAAAGAAAGAAAGTCC 1665
 QY 1604 TCAGAAAGCAGCTAAATTTCTCATACTATGTTTGTGCAAAACAGTAAAGATGGGGTAAAGT 1663
 Db 1666 TTTCTGAA-----CAATAAATACTTTAGTACTGTAGATATCCAGAAAGTGTCTTAAT 1719
 QY 1664 TCACCTATACAAACTCAAAAATTCAGAGATCAGTTCCAGAAATTTCTAGAGAGTACA 1723
 Db 1720 TTACCAACAGCAAAATTTGACTTTTAAATGAAGAGTATACCAAAAATAAACAAGAAATG 1779
 QY 1724 AAAGCTGTCAAGAAAGAAATTTGTAGCTGTGTAGTTTCAAAACAGCTGCGAGTTTCTCCAGG 1783
 Db 1780 AAGAAGCCAGGATGCCAATTTGTAAGAAATTTGTCAATAATTTCTTCAGGCTATGTAGAAC 1839
 QY 1784 TGTGTGAGGTATAGCTGGTGTACTTGTGATGTTGATGTTGATGTTGATGTTGATGTTG 1843
 Db 1840 CAATGCAGACACTCAATGATGTTGTAGCTCAGCTAGATGCTGTTGTGCTAGCTTTGCTCAG 1899
 QY 1844 TGGCTGCCAGTTGCCCACTCCCTACACAGCAACCAATATCAGTCCACCATACAGAG 1903
 Db 1900 TGTCAATGGAGCACCTGTTCCATATGTACGACCAAGCAATTTTGGAGAAAGCAAGGAA 1959

QY 1904 ATATTATCTTGAAGGGTGTAGGCATCTTGTGTGAAGCTCAAGATTGGGTTAACTCCA 1963
 Db 1960 GAATTATATTAAGAGCATCCAGGCACTGTTGTGTGAAGTTCAAGATGAATTTGCAATTA 2019
 QY 1964 TTCTTAATGACTGTAGACTAGTTTAGGGAGAGAGTTGGTTTCAGATATATCACAGGCCCTA 2023
 Db 2020 TTCTTAATGACGTATATCTTTGAAAAGATAAACAAGATGTTCCACATCATTTACTTGGCCCCA 2079
 QY 2024 ACATGGGTGGAAGTGCACCTACATTCGGCAGAGTTGGTGTGATGTCCTGATGCGCCCAAG 2083
 Db 2080 ATATGGGAGGTAAATCAACATATATTCGACAACTGGGGTGTAGTACTCATGCGCCAAA 2139
 QY 2084 TTGGCTCGTTTGTTCATGTGCAATTCATCTTCTATTCGTGATTTGATTTTGGCTC 2143
 Db 2140 TTGGGTGTTTGTGCCATGTGAGTCAGCAGAACTGTCATTTGGAGTGCATCTTAGCCC 2199
 QY 2144 GTGTTGGCGCTGGAGATGTCAGCTCAGAGGAGTTTCTACTTTTATGCAAGAGATGCTTG 2203
 Db 2200 GAGTAGGGGCTGGTGCAGCTCAATTTGAAAGGAGTCTCCAGTTTCATGGCTGAAATGTTGG 2259
 QY 2204 AGACTGCATCGATCTTGAAGGAGCTACTGATAGATCATTTGATTAATTTGATGAGTTGG 2263
 Db 2260 AACTGCTCTTATCTCAGGTCTGCAACCAAGATTCATTAATCAATAGATGAATGG 2319
 QY 2264 GCGTGGGACATCAACTACGATGGCTTTGGTTTAGCTTTGGGCTATTTGTGACACATTG 2323
 Db 2320 GAAGAGAACTTCTACTACGATGGATTTGGGTTAGCATGGGCTATCAGATACATTG 2379
 QY 2324 TTGAAGAAATTAAGCAACAATGTTTGGCCACTCACTTTTCATGAGCTGACTGCAATTAG 2383
 Db 2380 CAAACAAGATTTGGTGTCTTTTTCATGTTTGCACCACTTTTCATGAACCTTACTGCTTGG 2439
 QY 2384 CCAACAAGATGGAGACAATGGACATAAGAAATATCTGGGATAGCAAAATTTTCATGTTT 2443
 Db 2440 CCAATCAG-----ATACCACTGTTAATATCTACATGCTCA 2475
 QY 2444 TTGCACACATTTGACCTCTTAATCGCAAGCTACTATGCTTTTACAAGTTTCAACAGGTG 2503
 Db 2476 CAGCACTCA-----CCACTGAAGAGACCTTAATATGCTTTTATCAGGTGAAGAAAGGTG 2529
 QY 2504 CTTGTGATCAGATTTTGGTATTTCATGTTGCTGAAATTTGCAAAATTTTCCACCGAGTTG 2563
 Db 2530 TCTGTGATCAAGTTTGGGATTCATGTTGAGAGCTTGTCTAATTTTCCCTTAAGCATGTAA 2589
 QY 2564 TGCTCTGCTGAGAGAAAGGCACTGAGTTGGAGGATTTCTCTCTATTTGCTCAATATTC 2623
 Db 2590 TAGAGTGTGCTAAACAGAAAGCCCTGGAACCTGAGGATTTGAGTATATTGGAGATCGC 2649
 QY 2624 CAAATGACATTAAGAGGAGCTTCAAAAACGGAAGAGAGAAATTTGA 2669
 Db 2650 AAGGATATGATATCATGGAACAGCAGCAAGAAAGTGTATCTGGA 2695

RESULT 8

US-09-512-250C-1
 ; Sequence 1, Application US/09512250C
 ; Patent No. 6518042

GENERAL INFORMATION:

; APPLICANT: Borchert, Torben
 ; APPLICANT: Pedersen (Executor for Lars Christiansen, deceased), Dennis
 ; APPLICANT: Vind, Jesper
 ; TITLE OF INVENTION: A process for Making DNA Libraries in Filamentous Fungal Cells
 ; TITLE OF INVENTION: Cells
 ; FILE REFERENCE: 5718.200-US
 ; CURRENT APPLICATION NUMBER: US/09/512,250C
 ; CURRENT FILING DATE: 1999-02-24
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1
 ; LENGTH: 3823
 ; TYPE: DNA
 ; ORGANISM: Aspergillus oryzae


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FEATURE:
; NAME/KEY: CDS
; LOCATION: (700)..(723)
; OTHER INFORMATION:
;
FEATURE:
; NAME/KEY: CDS
; LOCATION: (781)..(3576)
; OTHER INFORMATION:
;
FEATURE:
; NAME/KEY: Intron
; LOCATION: (724)..(780)
; OTHER INFORMATION:
;
US-09-512-250C-1

Query Match      11.0%; Score 335; DB 4; Length 3823;
Best Local Similarity 49.4%; Pred. No. 8e-91;
Matches 1055; Conservative 0; Mismatches 1050; Indels 30; Gaps 6;

QY 493 GTTGGCTTAGGCTATGTTGATATTACTAAGAGAGTCCCTTGGTTTAAACAGAAATTTCTAGAT 552
DB 1225 GTGGAGTGTGCTTTGGGACGCAAGTGTACGGAACTCGGTGTTAGCGAGTTTCTGGAT 1284
QY 553 GATAGCCACTTCACAAATTTGGAGTCTGCTTTGGTTGCTCTTGGTTGCGAGAAATGCTTT 612
DB 1285 AAGCATATCTATTCCAACTTTGAGTCGCTTATTATCCAACTCGGGGTGAAGGAGTGTG 1344
QY 613 GTACCAAGCGGAGCTGGCAATCCAGTGAATACAGCCCTATGTTTGAATATC---T 669
DB 1345 GTGCAGATGATGCTAATAGAGAGTGTGAGCTGGGAAGATTCGGGCTATTGCGGAT 1404
QY 670 AGATGGCGGCTGATGTTAACTGAAAGAAAGAAACCTGAAATTTAAAGGAGAGATTTGGTA 729
DB 1405 AGTTGGGATCGCTATCTCCGAGAGCGGCTGCTGATTTATGGTGTCAAGATATTGAG 1464
QY 730 CAGGATCTTGGTAGGCTCGTCAAGGTTGAGTAGAACCTGTTGAGATTTGTTCTGCGG 789
DB 1465 CAGGATCTGACGAGGTTGTTGAGGAGTGAACGCTCGGCTGCTGACGCTGCGGACGAG 1524
QY 790 TTCGAATGTGATCAGGCGCTTTGGGTCATCTTTCTTATGCGAACTACTTGGCGAT 849
DB 1525 CTAAAGCTTGGATGGGCTCGGCGTCTGGTGTGATCAAGTACTCTTGGGCTTATGCGGAT 1584
QY 850 GAGAGCAACTTGAAGAACTATACAGTCAAAACATAACAACTCAATAGTTTACATGAGATTA 909
DB 1585 CCTACAACTTCGGCCAGTACCAAGCTCTATCAGCATGATTTGTCGCGAGTTTATGAGTTG 1644
QY 910 GATTCGTGCTATGAGAGACATGAATGTTAGGAGAGCAATCAGATGCTAATAAAT 969
DB 1645 GATTCGTGCGCGCTGCGTCTCTTAACTTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1704
QY 970 TTTAGCTTCTCGGCTGATGAATAGAACGTGTACTGCTGGAATGGTAAAGGTTATTG 1029
DB 1705 ATGAGTTTGGTTTGTGATCATCTGCAAGACCCCTG---TTGGTAGCCGTTGCTT 1761
QY 1030 CACATGTGCTGAAGCAACTTTTACTAGATGTAGAGAGATTAATCTGAGGCTGGATTTA 1089
DB 1762 GCGCAGTGGCTGAAAACAGCGGTGTGAGTCTGCGGAGATCGAGAGAGACAGCGCTT 1821
QY 1090 GTTCAATCACTGTTGAGAGATGCTGGCTTCCGCAAGATTT---GAGGCAAGATCTGAAA 1146
DB 1822 GTTGGGCGCTGTTGTTTAAACAGGAGCTCAGACAGACTATGAGGAGGAGATCTTCG 1881
QY 1147 AGAATTTCAAGATTTGAGCGGCTGACACAACTTTGAGAGGAAAGACCCAGTTTAGTG 1206
DB 1882 TCCATACCGGATCTGTATAGACTAGGAGAGCGGTTCACGGCAACAGGCAACTTTGGAA 1941
QY 1207 CAGGTTGTAAGAACTCTATCAGTCAAGTACCAGAGTACCATATATCAAAAGTGTTTGGAA 1266
DB 1942 GAGGTTGTGGGCTGTACCAAGTGTGCTATTCTGTTGCTGTTTGTCACTCTCTCGAG 2001
QY 1267 CGTCATGATGGGCAATTTGCAACATCTCATGAGGAAAGGATATTGATTTCTCTAGAGAA 1326
DB 2002 AATGTTATGATGATGAGAGTATCAGACGCGCCCTGGAGACGGA---GTATACTTCCAACTC 2058

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QY 1327 TGGAGTGATGATAATCACTGAATAGTTCAATAGTCTTTGTGGAACCTTCTGTGACCTT 1386
DB 2059 CGGAGTCACTCTGATAGCTTAGCGAACTGGAGGAGATGGTTGAGACTACGGTTGACCTT 2118
QY 1387 GATCAACTTTGAGAAATGAGAAATACATGATTTCTTCTGCAATATGACCAAAATTTATCTGCT 1446
DB 2119 GATGCGCTGAGAACCAAGGTTTCAATCAAGCCTGAGTTTGAACGAGAGTCTGCGGATC 2178
QY 1447 CTGAAGGATGAGCAAGAGACATTTGGAGCGACAAATTCATAATTTTGCAAAAACAACTGCC 1506
DB 2179 ATCAGGAAGAACTGGCAAGCTCCGTATGATATGGCGTTGAGCACCGCAGGGTAGCT 2238
QY 1507 AATGATCTGTACTTACTTATGATTAAGTCACTTAACCTAGATAAAGAAACAACTTTGGA 1566
DB 2239 CGGAGCTTTGACCAAGATATTGAGAAGAGTTGTTCTCTGGAAGAACACAGGGGTGACGGA 2298
QY 1567 CACGCTCTTCCAGAAATACCAAGAAAGAAACAAAGAGTCAAGAGCAGCTAAATTTCTCAC 1626
DB 2299 TGGTCTTCCGACTTACTCGCAACGAGTCGGGATGCATCCGCAATAGAGAGATACAG 2358
QY 1627 TACATTTGTTCTCGAAACACGTAAGGATGGGTAAGTTTCACTTATACAAACCTCAAAAA 1686
DB 2359 GAATGTTCT-----ACACAGAAAGAAAGGTTCTACTTCACTACGTCGACTATGCAAAAC 2412
QY 1687 CTAGGAGATCAGTTCAGNAGAGATTGTAGAGGAGTACAAAGCTGTGAGAAAGATTTGTA 1746
DB 2413 TTGCGCGGAGCATGATCACTGCTCGAACTCAATAGAACTCAGACCCGCGCTGGTG 2472
QY 1747 GCTGTGTAGTTTCAAAACAGCTCGGAGTTTCTCCGAGGTGTTTGCAGGTATAGCTGGTGA 1806
DB 2473 AATGAGTCTGTTAAAGTTGCGCGCTCTACTGCTCTGTTTGGACGACTTSCGGTGTG 2532
QY 1807 CTTGTGAGTTGGATGTTTACTGAGTTTTCGAGTTTTCGAGTTTTCGCTGCCAGTTGCCAACCTCC 1866
DB 2533 ATAGCACACCTCGATGTCATTTAAAGTTCGCTCATGCTCTGTTCTCATGCGCGACCC 2592
QY 1867 TACACAAGACCAAAATCAGTCCACAGATACAGAGATATTTATCTTGAAGGTTGATG 1926
DB 2593 TATGTCGCGCCCAAGATGCCACCCGAGGACCCGGAACACAGATTTCTCAAGAAAGCGCG 2652
QY 1927 CATCTGTGTGGAAGCTCAAGATTTGGGTTAACTCCATTCCTAAAGTGTAGACTAGTT 1986
DB 2653 CACCCCTGTATGGAATAGCAGATGATATTTCAATTCATTAATGATGCTGCTTGGTGTG 2712
QY 1987 AGGGAGAGAGTTGTTTTCAGATTTATCAGGCCCTTAACATGGGTGGAAGTTCGACCTAC 2046
DB 2713 CGAGACGAGTCTCTCTTCTCATCTATCTGCTTAACTGCTTAACTGCGAGGTTAAATCGACTAT 2772
QY 2047 ATTGCGGAGGTTGGTGTGAATGTCCTGATGGCCCAAGTTGGCTGCTTTGTTTCCATGTGAC 2106
DB 2773 ATTCCCAAAATTTGGTGTATGCTCTCATGCTCAGACGGGCTGCTTTGTGCTTTGTA 2832
QY 2107 AATGCTACCAATTTCTGATTTGATTTGTTGCTCGTTTGGGCTGGAGATTCGAC 2166
DB 2833 GAGCAGAAATTTGACCATCTTTGACTGTATCTTGCACGTTGTTGGTGAAGTGTATCAGAG 2892
QY 2167 CTGAGAGGAGTTTCTATCTTTTATGCAAGAGATGCTGTGAGATGCTGATTCGATCTTGAAGA 2226
DB 2893 CTCAAGGGAGTTTCCACTTTTCATGCTGAGATGCTCGAAACATCCAACTCTCAAGTCG 2952
QY 2227 GCTACTGATAGATCATCTTATGATTTATGATGAGTTGGCGCGGTGGGACATCACTTACGAT 2286
DB 2953 GCACTCGAGTCTCTTATCATCATGACGAGCTTGGCGCGGTGACAGCAGTATGAC 3012
QY 2287 GGTCTTGGTTTGTAGCTTGGGCTATTTGTGAGCACAATTTGTGAAGAAATTAAGCAACA 2346
DB 3013 GGAATTCGCGCTAGCATGGCCATCTCTGAACATCTGTCAGAGATTCGTTGCTTCGCG 3072
QY 2347 TTGTTTGCACCTCACTTTCTGATGAGCTGTGATTTAGCCAAACAGAAATGGAGAGAAATGA 2406
DB 3073 CTTTTCGCTACTCACTTCCATGAATTTGACGCTCTCGCGGATCGATACCCCAAGTCTGTC 3132

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QY 2407 CATAGAAAAATG-----CTGGATAGCAAAATTTTCATGTTTTCACACATT 2454
 Db 3133 AAGAACTGCGAGTAGTGGCTTTCATCGCGATGCTGATGATGACAGTGAAGTAAG 3192
 QY 2455 GACCTTCTTAATCGAAGCTAAGTTTACAGGTTTACAGGTTTCCAGGTTGTTGATCAG 2514
 Db 3193 AAGTCCAAAGCGAAGCAAGTCTACTTCTGTACCGGTCGAACCTGGCAATTTGTGCCAG 3252
 QY 2515 AGTTTGTGTTTTCATGTTGCTGAATTTGCAAAATTTCCACCGAGTGTGTTGGCTCTGCT 2574
 Db 3253 TCATTCGATTCACCGTTGCCGAATTTGTCGCTTCCCGGAAGAGTGTGCAATGSCC 3312
 QY 2575 AGAGAAAAGGCTCTGAGTTGGAGGATTTCTCTCC 2609
 Db 3313 GCCAGAGGAGAGGAACTTGAAGACTTTACTTC 3347

RESULT 9
 US-09-651-656-2
 ; Sequence 2, Application US/09651656
 ; Patent No. 6340566
 ; GENERAL INFORMATION:
 ; APPLICANT: MCCUTHEN-MALONEY, SANDRA
 ; APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
 ; TITLE OF INVENTION: DETECTION AND QUANTITATION OF SINGLE NUCLEOTIDE
 ; TITLE OF INVENTION: POLYMORPHISMS, DNA SEQUENCE VARIATIONS, DNA MUTATIONS,
 ; TITLE OF INVENTION: DNA DAMAGE AND DNA MISMATCHES
 ; FILE REFERENCE: IL-10689
 ; CURRENT APPLICATION NUMBER: US/09/651,656
 ; CURRENT FILING DATE: 2000-08-29
 ; PRIOR APPLICATION NUMBER: 60/192,764
 ; PRIOR FILING DATE: 2000-03-28
 ; NUMBER OF SEQ ID NOS: 106
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 723
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-651-656-2

Query Match 7.7%; Score 234; DB 4; Length 723;
 Best Local Similarity 59.8%; Pred. No. 1.2e-60;
 Matches 446; Conservative 0; Mismatches 270; Indels 30; Gaps 2;
 QY 1924 AGGCATCTTGTGTGGAGCTCAAGATTGGGTTAACTCCATTCTTAATGACTGTAGACTA 1983
 Db 4 AGGCATCTTGTGTGGAGCTCAAGATTGGGTTAACTCCATTCTTAATGACTGTAGACTA 63
 QY 1984 GTTATGGGAGAGAGTTGGTTTCAGATTATACAGGCCCTCAACATGGGTGGAAAGTCGACC 2043
 Db 64 GAAAAGATATAACAGATGTTCCACATCATTTACTGGCCCCCATATGGAGGTAAATCAACA 123
 QY 2044 TACATTCGGCAGGTTGGTGTGAATGCTGATGGCCCAAGTTGGCTCGTTTGTTCATGT 2103
 Db 124 TATATTGCAAACTGGGGTGATAGTACTCATGCCCAAAATGGGTGTTTGTGCCATGT 183
 QY 2104 GACAAATGCTACCATTTCTATTCTGATTTGTTTGTCTGTTGCGCTGGAGATTGC 2163
 Db 184 GAGTCAGCAGAGTGTCCATTGTGGACTGCTATTCAGCCGAGTAGGGCTGGTGAAGT 243
 QY 2164 CAGTCAGAGAGGTTTCTACTTTTATGCAAGAGATGCTTCAGACTGCTCATCTTCAAA 2223
 Db 244 CAATTGAAAGAGGTCCTCCAGTTTCATGGCTGAATGTTGAAACTGCTTCTATCTCAGG 303
 QY 2224 GGAGTACTGATAGTATCATTTATATTAATGATGAGTTGGCCGCTGGACATCAACCTAC 2283
 Db 304 TCTGCAACCAAGATTCATTAATTAATCATAGATGAATTTGGAAGAGGAACTTCTACCTAC 363
 QY 2284 GATGCTTTGGTTAGCTTTGGGCTATTTGTGAGCAGCATTTGTTGAAGAAATTAAGCACCA 2343
 Db 364 GATGAATTTGGTTAGCATGGCTATATCATGAATACATTGCAACAAGATTTGGTCTTTT 423
 QY 2344 ACATTTTGGCACTCACTTTTCATGAGCTGATGCTATTTAGCCAAACAAGATGGAGACAAT 2403

Db 424 TGCATGTTTCAACCCATTTTCATGACTTACTGCTTGGCCATCAGATCAACACTGTT 483
 QY 2404 GGACATAGAAAATGCTGGATAGCAAAATTTTCATGTTTTCACACATTGACCTTCT 2463
 Db 484 AAT-----AATCTACATGTCACAGCACTCA-----CCACT 513
 QY 2464 AATCGCAAGCTAACTATGCTTTTACAAAGTTTCAACCGAGTGTCTGTGATCAGAGTTTGGT 2523
 Db 514 GAAGAGACCTTAATGCTTTTATCAGTGAAGAAAGTGTCTGTGATCAAAATTTGGG 573
 QY 2524 ATTCAATGCTGTAATTTGCAAAATTTTCCACCGAGTGTGTGGCTCTGGCTAGAGAAAAG 2583
 Db 574 ATTCATGTTGCAGAGCTTGTCTAATTTCCCTAAGCATGTAATAGAGTGTGCTTAAACAGAAA 633
 QY 2584 GCATCTGAGTTGGAGGATTTCTCTCTATTGCCCATAATTCCAATGATCAATTAAGAGGCA 2643
 Db 634 GCCCTGGAACCTTGAGGAGTTTCAGTATATTGGAGATCGCAAGGATATGATATCATGGAA 693
 QY 2644 GCTTCAAAACGGAAGAGAGAAATTTGA 2669
 Db 694 CCAGCAGCAAGAAGTCTATCTGGA 719

RESULT 10
 US-09-650-855-2
 ; Sequence 2, Application US/09650855
 ; Patent No. 6365355
 ; GENERAL INFORMATION:
 ; APPLICANT: MCCUTHEN-MALONEY, SANDRA
 ; APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
 ; TITLE OF INVENTION: CHIMERIC PROTEINS FOR DETECTION AND QUANTITATION OF DNA
 ; TITLE OF INVENTION: MUTATIONS, DNA SEQUENCE VARIATIONS, DNA DAMAGE AND DNA
 ; TITLE OF INVENTION: MISMATCHES
 ; FILE REFERENCE: IL-10284
 ; CURRENT APPLICATION NUMBER: US/09/650,855
 ; CURRENT FILING DATE: 2000-08-29
 ; PRIOR APPLICATION NUMBER: 60/192,764
 ; PRIOR FILING DATE: 2000-03-28
 ; NUMBER OF SEQ ID NOS: 106
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 723
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-650-855-2

Query Match 7.7%; Score 234; DB 4; Length 723;
 Best Local Similarity 59.8%; Pred. No. 1.2e-60;
 Matches 446; Conservative 0; Mismatches 270; Indels 30; Gaps 2;
 QY 1924 AGGCATCTTGTGTGGAGCTCAAGATTGGGTTAACTCCATTCTTAATGACTGTAGACTA 1983
 Db 4 AGGCATCTTGTGTGGAGCTCAAGATTGGGTTAACTCCATTCTTAATGACTGTAGACTA 63
 QY 1984 GTTATGGGAGAGAGTTGGTTTCAGATTATACAGGCCCTCAACATGGGTGGAAAGTCGACC 2043
 Db 64 GAAAAGATATAACAGATGTTCCACATCATTTACTGGCCCCCATATGGAGGTAAATCAACA 123
 QY 2044 TACATTCGGCAGGTTGGTGTGAATGCTGATGGCCCAAGTTGGCTCGTTTGTTCATGT 2103
 Db 124 TATATTGCAAACTGGGGTGATAGTACTCATGCCCAAAATGGGTGTTTGTGCCATGT 183
 QY 2104 GACAAATGCTACCATTTCTATTCTGATTTGTTTGTCTGTTGCGCTGGAGATTGC 2163
 Db 184 GAGTCAGCAGAGTGTCCATTGTGGACTGCTATTCAGCCGAGTAGGGCTGGTGAAGT 243
 QY 2164 CAGTCAGAGAGGTTTCTACTTTTATGCAAGAGATGCTTCAGACTGCTCATCTTCAAA 2223
 Db 244 CAATTGAAAGAGGTCCTCCAGTTTCATGGCTGAATGTTGAAACTGCTTCTATCTCAGG 303
 QY 2224 GGAGTACTGATAGTATCATTTATTAATGATGAGTTGGCCGCTGGACATCAACCTAC 2283

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Db 304 TCTGCAACCAAGATTCAATTAATCATAGATGAATTTGGGAAGAGGAACTTCTACCTAC 363
QY 2284 GATGGCTTTGGTTAGCTTGGGCTATTTGTGAGCACAATTGTTGAAGAAATTAAGACCA 2343
Db 364 GATGGATTTGGGTTAGCATGGGCTATATCAGATACATTCGAAACAAGATTGGTGCTTT 423
QY 2344 ACATTTGTTGCCACTCACTTTTCATGAGCTGACTGCACTAGCCCAACGAAGATGGAGCAAT 2403
Db 424 TGCAATGTTGCAACCACTTTTCATGACTTACTGCTTGGCCCAATCAGATACCACTGTT 483
QY 2404 GGCATTAAGAAAATGCTGGGATAGCAAAATTTCAATGTTTTTGCACATGACCCCTTCT 2463
Db 484 AAT-----AATCTACATGTCACAGCACTCA-----CCACT 513
QY 2464 AATCGCAAGCTAACTATGCTTTACAAAGTTTCAACAGGTTTCAACAGGCTGCTGTGATCAGATTTGGT 2523
Db 514 GAAGAGACCTTAATAGCTTTTATCAGGTGAAGAAAGGCTGCTGTGATCAAGTTTGGG 573
QY 2524 ATTCAATGTTGCTGAATTTGCAAAATTTTCCACCGAGTGTGCTGCTGCTAGAGAAAAG 2583
Db 574 ATTCAATGTTGACAGCTTGTCTAATTTCCCTAAGCATGTATAGAGTGTGCTTAACAGAAA 633
QY 2584 GCATCTGAGTTGAGAGATTTCTCTCCATTTGCCAATATTCCTAATGATCAATTAAGAGGCA 2643
Db 634 GCCTTGAACCTTGAGGAGTTTTCAGTATATTTGGGAATCGCAAGGATATGATATCATGGAA 693
QY 2644 GCTTCAAAACGGAAGAGAGATTGA 2669
Db 694 CCAGCAGCAAGAAGTCTATCTGGA 719

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RESULT 11

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US-08-956-171B-231/c
; Sequence 231, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: P248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 231:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 3159 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 231:
US-08-956-171E-231

Query Match 4.5%; Score 136.8; DB 4; Length 3159;
Best Local Similarity 51.1%; Pred. No. 8.9e-31;
Matches 380; Conservative 0; Mismatches 352; Indels 12; Gaps 2;

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Db 2066 CATTTAGTGAAATAAACAATTAGA-----ATTAGTGAATCTAGGCCACCCAGTAGTGG 2013
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Db 2012 AAAGATAATGGAATTAATGACTATGTGCTTAATAATTTGCGATTAGATAAATGAACAT 1953
QY 2000 GGTTCAGATTTACAGAGCCCTTAAACATGGGTGGAAGTCGACCTACATTCGCGCAGTTG 2059
Db 1952 TTATATATTTAATACAGGTCCGAATATGTCGTGTAATCGACATATATGAGACAAGTTG 1893
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QY 2120 CTATTCGTGATTTGATTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2179
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QY 2180 CTACTTTTATGCAAGAGATGCTTTGAGACTGCTAGCTGCTTTGAAAGGAGCTACTGATAGAT 2239
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QY 2240 CATTGATTAATTAATGATGAGTTGGCGCTGGGAGCATCAACCTACGATGCTGTTGTTAG 2299
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QY 2300 CTTGGGCTATTTGTGAGCACAATTTGTAAGAAATTAAGACCAACCAATTTGTTGCCACTC 2359
Db 1652 CGCAGGCAATGATAGAGTATGTAGCTGAAACATCAGATGCTAAGACGTTATTTTCAACAC 1593
QY 2360 ACTTTCATGAGCTGACTGCAATTAG 2383
Db 1592 ATTATCATGAATTCACAACATTAG 1569

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RESULT 12

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US-08-743-637B-31
; Sequence 31, Application US/08743637B
; Patent No. 5994066
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: PICARD, Francois J.
; APPLICANT: OUELLETTE, Marc

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APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: QUARLES & BRADY
STREET: 411 EAST WISCONSIN AVENUE
CITY: MILWAUKEE
STATE: WISCONSIN
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,637B
FILING DATE: 04-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,840
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586.90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 3754 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae

Query Match 4.5%; Score 135.8; DB 2; Length 3754;
Best Local Similarity 52.6%; Pred No. 2e-30;
Matches 349; Conservative 0; Mismatches 302; Indels 12; Gaps 2;
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QY 2194 GAGATGCTTGAGACTGCGATCGATCTTGAAGAGCTACTGATAGATCATTGATTATATT 2253
DB 2951 GAGATGATGGAGGCCAATAATGCCATTTCCGATCGGACCAAGAACTCTCTCTCTCTTT 3010
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DB 3071 GAATATATCCATGAGCACATCGGAGCTAAGACCCTCTTTGGGACCCACTACCATGAGTTG 3130
QY 2374 ACT 2376
DB 3131 ACT 3133

RESULT 13

US-08-526-840B-31
Sequence 31, Application US/08526840B
Patent No. 6001564
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE
GENES FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
NUMBER OF SEQUENCES: 177
CORRESPONDENCE ADDRESS:
ADDRESSEE: QUARLES & BRADY
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,840B
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/304,732
FILING DATE: 12-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586.90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 3754 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
US-08-526-840B-31

RESULT 15

US-09-543-681A-2786
 ; Sequence 2786, Application US/09543681A
 ; Patent No. 6605709
 ; GENERAL INFORMATION:
 ; APPLICANT: GARY BRETON
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
 ; FILE REFERENCE: 2709.1002-001
 ; CURRENT APPLICATION NUMBER: US/09/543.681A
 ; CURRENT FILING DATE: 2000-04-05
 ; PRIOR APPLICATION NUMBER: US 60/128,706
 ; PRIOR FILING DATE: 1999-04-09
 ; NUMBER OF SEQ ID NOS: 8344
 ; SEQ ID NO 2786
 ; LENGTH: 2625
 ; TYPE: DNA
 ; ORGANISM: Proteus mirabilis
 US-09-543-681A-2786

Query Match		4.4%	Score 132.8;	DB 4;	Length 2625;
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Qy	1982	TAGTTAGGGAGAGAGTGGTTTCAGATTATCACAGGCCCTTAACATGGGTGGAAAGTCGA	2041		
Db	1868	AACTCGGCCCTCAACGCGCTCTACTATTATACCGGCCCTTAATGCGGCTAAAGTA	1927		
Qy	2042	CCTACATTCGCGAGTGGTGTGAATGCTCTGATGCGCCCAAGTTGGCTCGTTGTTCCAT	2101		
Db	1928	CCTATATGCGTCAAGCGGCATTAATTACGCTACTCGGCTTATATTGGTAGTTTTTGTGCGCG	1987		
Qy	2102	GTGACATGCTACCATTTCTATTCGTGATTGTTATTTTGTCTCGTGTGGCGCTGGAGATT	2161		
Db	1988	CAGAAAAGCGGTAAATAGGCCCAATTGATCGTATTTTTTACCCGCGTGGTGCCTCTGACG	2047		
Qy	2162	GCCAGCTGAGAGGAGTTTCTACTTTTATGCAAGAGATGCTTGAGACTGCATCGATCTTGA	2221		
Db	2048	ATCTGGCTTCGGTTCGTTCAACATTTATGGTGGAAATGACAGAAACCGCAATATCCTTC	2107		
Qy	2222	AAGGAGCTACTGATAGATCATTTGATTAATAATGATGAGTTGGCGCTGGGACATCAACCT	2281		
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Qy	2342	CAACATTTGTTGCCACTCACCTTTTCATGAGCTGACTGCATTAGCCCAAGAAATGGAGACA	2401		
Db	2228	TGACACTCTTTGCCACACACTATTTTGAATTAACGACACTGCCAGAAAACACTAGAAGCA	2287		
Qy	2402	ATGACATTAAGAAAAATGCTGGGATAGCAAAATTTTCATGTTTTCACACATTGAC	2457		
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Search completed: April 9, 2004, 06:53:04
 Job time : 216 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2004, 06:45:13 ; Search time 1017 Seconds
(without alignments)
11187.987 Million cell updates/sec

Title: US-10-029-065-1

Perfect score: 3033

Sequence: 1 ataaaggttaagaaaaa.....tatcttatatgtcacaataa 3033

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2475585 seqs, 1875730760 residues

Total number of hits satisfying chosen parameters: 4951170

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications NA:

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18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1063.2	35.1	2151	12	US-10-424-599-71262
5	825	27.2	1954	12	US-10-425-114-12569
6	706.4	23.3	1723	12	US-10-425-114-3918
7	685.8	22.6	5307	14	US-10-270-839-48
8	627.6	20.7	1124	12	US-10-424-599-141791
9	422.4	13.9	3080	14	US-10-171-581-78
10	422.4	13.9	3161	15	US-10-062-674-1794
11	420.8	13.9	2805	14	US-10-109-791A-3
12	420.8	13.9	3145	9	US-09-788-657-9
13	420.8	13.9	3145	10	US-09-912-697-9
14	420.8	13.9	3145	10	US-09-760-285-21
15	420.8	13.9	3145	12	US-10-342-887-455

16 420.8 13.9 3145 14 US-10-270-839-30 Sequence 30, Appl
17 420.8 13.9 3145 14 US-10-243-130-12 Sequence 12, Appl
18 420.8 13.9 3145 14 US-10-371-857-15 Sequence 15, Appl
19 420.8 13.9 3145 14 US-10-371-634-10 Sequence 10, Appl
20 420.8 13.9 3145 14 US-10-348-074-8 Sequence 8, Appl
21 420.8 13.9 3145 14 US-10-369-845-14 Sequence 14, Appl
22 291.4 9.6 2793 15 US-10-369-493-27560 Sequence 27560, A
23 288.4 9.5 2895 15 US-10-369-493-25709 Sequence 25709, A
24 288.4 9.5 2901 14 US-10-109-791A-2 Sequence 2, Appl
25 186.2 6.1 403 15 US-10-062-674-1322 Sequence 1322, Ap
26 168.6 5.6 311 14 US-10-029-065-15 Sequence 15, Appl
27 165.4 5.5 314 14 US-10-029-065-14 Sequence 14, Appl
28 163 5.4 2547 12 US-10-282-122A-36266 Sequence 36266, A
29 160.8 5.3 2847 12 US-10-282-122A-16980 Sequence 16980, A
30 159 5.2 314 14 US-10-029-065-13 Sequence 13, Appl
31 151.4 5.0 2523 15 US-10-369-493-42208 Sequence 42208, A
32 150.8 5.0 2589 12 US-10-282-122A-11088 Sequence 11088, A
33 146.6 4.8 2463 12 US-10-282-122A-18909 Sequence 18909, A
34 144.8 4.8 2613 9 US-09-815-242-4219 Sequence 4219, Ap
35 144.8 4.8 2619 9 US-09-815-242-8235 Sequence 8235, Ap
36 141.8 4.7 2556 12 US-10-282-122A-38621 Sequence 38621, A
37 140.2 4.6 2526 15 US-10-369-493-33427 Sequence 33427, A
38 137.6 4.5 2562 12 US-10-282-122A-32738 Sequence 32738, A
39 136.8 4.5 2325 12 US-10-282-122A-8190 Sequence 8190, Ap
40 136.8 4.5 3159 8 US-08-781-986A-231 Sequence 231, App
41 136.8 4.5 3159 12 US-10-329-624-231 Sequence 231, App
42 136.8 4.5 3521 14 US-10-270-839-50 Sequence 50, Appl
43 135.8 4.5 2535 9 US-09-815-242-9417 Sequence 9417, Ap
44 135.8 4.5 2574 12 US-10-282-122A-38017 Sequence 38017, A
45 135.8 4.5 3754 9 US-09-452-599-31 Sequence 31, Appl

ALIGNMENTS

RESULT 1

US-10-029-065-1
; Sequence 1, Application US/10029065
; Publication No. US20030150024A1
; GENERAL INFORMATION:
; APPLICANT: May, Gregory
; APPLICANT: Baszczyński, Christopher
; APPLICANT: Zhu, Tong
; APPLICANT: Kipp, Peter
; APPLICANT: Mahajan, Pramod
; TITLE OF INVENTION: PLANT MSH2 SEQUENCES AND METHODS OF USE
; FILE REFERENCE: 5839-2 (035839/196219)
; CURRENT APPLICATION NUMBER: US/10/029,065
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent version 3.0
; SEQ ID NO 1
; LENGTH: 3033
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22)..(2838)
US-10-029-065-1

Query Match 100.0%; Score 3033; DB 14; Length 3033;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3033; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAAAGGTTAAAGAAAAAATGAATGAAAAATTTGGAGGAAACAGACGAAGCTTCCCGAG 60

Db 1 ATAAAGGTTAAAGAAAAAATGAATGAAAAATTTGGAGGAAACAGACGAAGCTTCCCGAG 60

QY 61 CTTAAACTGGATGCTAAGCAAGCTCAAGATTCTCTCATTTCTTCAAAACCTGCCCAAG 120

Db 61 CTTAAACTGGATGCTAAGCAAGCTCAAGATTCTCTCATTTCTTCAAAACCTGCCCAAG 120

QY 121 GACCCCTAGGGCAGTTCCGCTCTTTGATCGTCGGGACTATTATACATCTCTCATGGAGATGAT 180

121 GACCTTAGGCGAGTTCGCTCTTTTGATGTCGCGAATTAATATACATCTCATGAGAGAT 180
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1681 AAAAACTAGGAGATCAGTTCCAGAAAGATTTGTAGAGAGGTACAAAAGCTGTTCAGAAAGAA 1740
1741 TTGGTAGCTCGTGTAGTTCAACAGCTGCGAGTTTCTCCGAGGTGTTTCAGGTATAGCT 1800
1741 TTGGTAGCTCGTGTAGTTCAACAGCTGCGAGTTTCTCCGAGGTGTTTCAGGTATAGCT 1800
1801 GGTGTACTTGTGAGTGTGATGTTTACTGAGTTTTCGGGATTTGCGGATTCGCTGCGGCTA 1860
1801 GGTGTACTTGTGAGTGTGATGTTTACTGAGTTTTCGGGATTTGCGGATTCGCTGCGGCTA 1860
1861 ACTCCCTACACAAGACCAATATCAGTCCACAGATACAGAGATATATACCTTGAAGGG 1920
1861 ACTCCCTACACAAGACCAATATCAGTCCACAGATACAGAGATATATACCTTGAAGGG 1920
1921 TGTAGGATCTCTTGTGGAAGCTCAAGATTTGGGTTAACTCCATTCCTAATGACTGTAGA 1980
1921 TGTAGGATCTCTTGTGGAAGCTCAAGATTTGGGTTAACTCCATTCCTAATGACTGTAGA 1980
1981 CTAGTTAGGGGAGAGTGGTTTTCAGATTTATCAAGGCCCTTAACTGCGTGGTGGAAAGTCG 2040
1981 CTAGTTAGGGGAGAGTGGTTTTCAGATTTATCAAGGCCCTTAACTGCGTGGTGGAAAGTCG 2040
2041 ACCTACATTCGGCAGGTGGTGTGAATGCTCATGCGGCCCAAGTTGGCTCGTTGTTTCCA 2100
2041 ACCTACATTCGGCAGGTGGTGTGAATGCTCATGCGGCCCAAGTTGGCTCGTTGTTTCCA 2100
2101 TGTGACAACTCTACCAATTTCTATTCGTTGATTTGTTTTCGTTGCGGCTGGAGAT 2160
2101 TGTGACAACTCTACCAATTTCTATTCGTTGATTTGTTTTCGTTGCGGCTGGAGAT 2160
2161 TGCAGCTGAGAGAGTTCCTACTTTATGCAAGAGATGCTTGGAGTCTGATCGATCTTG 2220
2161 TGCAGCTGAGAGAGTTCCTACTTTATGCAAGAGATGCTTGGAGTCTGATCGATCTTG 2220
2221 AAAGGAGCTACTGATAGATCAATTTGATTAATTTGATGAGTGGCGGTGGGACATCAACC 2280
2221 AAAGGAGCTACTGATAGATCAATTTGATTAATTTGATGAGTGGCGGTGGGACATCAACC 2280
2281 TAGCATGGCTTTGGTTTGTAGCTTGGGCTTATTTGTGAGCACTTGTGGAAGAAATTAAGCA 2340
2281 TAGCATGGCTTTGGTTTGTAGCTTGGGCTTATTTGTGAGCACTTGTGGAAGAAATTAAGCA 2340

1030 CACATGTCGCTGAGCAACCTTTTACTAGATCTAGAGAGATTAAGTCTGATTTA 1089
 Db
 1030 CACATGTCGCTGAGCAACCTTTTACTAGATCTAGAGAGATTAAGTCTGATTTA 1089
 Qy
 1090 GTTCAATCATTCGTGGAGATGCTGCGCTTCGCAAGATTTGAGGCAACATCTCAAAAGA 1149
 Db
 1090 GTTCAATCATTCGTGGAGATGCTGCGCTTCGCAAGATTTGAGGCAACATCTCAAAAGA 1149
 Qy
 1150 ATTTGAGATATGAGCGCTGACACACAAATCTTGAGAGAGAAAGAGCGATTTAGTGAC 1209
 Db
 1150 ATTTGAGATATGAGCGCTGACACACAAATCTTGAGAGAGAAAGAGCGATTTAGTGAC 1209
 Qy
 1210 GTTGTAAATCTATCAGTCAAGTACAGAGTACCATATATCAAAAGTGTGTTGGAAGT 1269
 Db
 1210 GTTGTAAATCTATCAGTCAAGTACAGAGTACCATATATCAAAAGTGTGTTGGAAGT 1269
 Qy
 1270 CATGATGGCAATTTGCAACACTCATCAGGGAAGGTATATGATTTCTTAGAGAAATGG 1329
 Db
 1270 CATGATGGCAATTTGCAACACTCATCAGGGAAGGTATATGATTTCTTAGAGAAATGG 1329
 Qy
 1330 AGTGAATATACCTGAATTAAGTTCTATAGTCTGTGGAATCTTCTGTTGACCTTGAT 1389
 Db
 1330 AGTGAATATACCTGAATTAAGTTCTATAGTCTGTGGAATCTTCTGTTGACCTTGAT 1389
 Qy
 1390 CAATCTGAGATGAGATATGATTTCTTCTGATATGACCCAAATTTATCTGCTCTG 1449
 Db
 1390 CAATCTGAGATGAGATATGATTTCTTCTGATATGACCCAAATTTATCTGCTCTG 1449
 Qy
 1450 AAGGATGAGCAAGAGACATTTGAGCGCAAAATTTCAATAATTTGCAAAACAAATGCGCAAT 1509
 Db
 1450 AAGGATGAGCAAGAGACATTTGAGCGCAAAATTTCAATAATTTGCAAAACAAATGCGCAAT 1509
 Qy
 1510 GATCTGATCTACCTATGATTAAGTCACTTAACTAGATAAGAAACAAATTTGGAAC 1569
 Db
 1510 GATCTGATCTACCTATGATTAAGTCACTTAACTAGATAAGAAACAAATTTGGAAC 1569
 Qy
 1570 GTCTTCAGAAATACCAAGAGAGAACCAAAAGTCAGGAGCAGTAAATTTCTCACTAC 1629
 Db
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 Qy
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 Db
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 Qy
 1690 GGAGATCAGTTCCAGAAATTTGAGAGATACAAAGCTGTCAGAAAGAAATTTGATGCT 1749
 Db
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 Qy
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 Db
 1750 CGTGTAGTTCAAAACAGCTGCGAGTTTCTCCGAGGTGTTGCAAGGTATAGCTGCTACTT 1809
 Qy
 1810 GCTGAGTTGGATGTTACTGAGTTTTCGGAATTTGGCTGCGAGTTGCCAACTCCCTAC 1869
 Db
 1810 GCTGAGTTGGATGTTACTGAGTTTTCGGAATTTGGCTGCGAGTTGCCAACTCCCTAC 1869
 Qy
 1870 ACAAGACCAATATACGTCACAGATACAGAGATATATATCTTGAAGGGTGTAGGCAT 1929
 Db
 1870 ACAAGACCAATATACGTCACAGATACAGAGATATATATCTTGAAGGGTGTAGGCAT 1929
 Qy
 1930 CTTGTGTGGAAGCTCAAGATTTGGGTAACTCCATTTCTATGACTGTAGACTAGTTAGG 1989
 Db
 1930 CTTGTGTGGAAGCTCAAGATTTGGGTAACTCCATTTCTATGACTGTAGACTAGTTAGG 1989
 Qy
 1990 GGAGAGATGTTGTTTTCAGATTAACAGGCCCTTAAATGAGTGGTGAAGTTCGACCTACAT 2049
 Db
 1990 GGAGAGATGTTGTTTTCAGATTAACAGGCCCTTAAATGAGTGGTGAAGTTCGACCTACAT 2049
 Qy
 2050 CGGAGGTTGGTGTGAATGCTGATGGCCCAAGTTGGCTGCTGTTTGTCCATGTGACAAAT 2109
 Db
 2050 CGGAGGTTGGTGTGAATGCTGATGGCCCAAGTTGGCTGCTGTTTGTCCATGTGACAAAT 2109

2110 GCTACCAATTTCTATTCGTGATTTGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2169
 Db
 2110 GCTACCAATTTCTATTCGTGATTTGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2169
 Qy
 2170 AGAGGAGTTTCTACTTTTATGCAAGAGATCTTTGAGACTGATCTTTGAAAGGAGCT 2229
 Db
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 Qy
 2230 ACTGATAGATCATTTGATTAATTTGATGAGTTGGGCGTGGGACATCAACTGATGAGTGC 2289
 Db
 2230 ACTGATAGATCATTTGATTAATTTGATGAGTTGGGCGTGGGACATCAACTGATGAGTGC 2289
 Qy
 2290 TTTGGTTTGTAGCTGGGCTATTTGTGAGCAATTTGTGAAGAAATTTAAAGCACCACCAATTG 2349
 Db
 2290 TTTGGTTTGTAGCTGGGCTATTTGTGAGCAATTTGTGAAGAAATTTAAAGCACCACCAATTG 2349
 Qy
 2350 TTTGCCACTCACTTTTCAATGAGTGAATTTGCAATGAGTGAATTTGCAATGAGTGAATTTCA 2409
 Db
 2350 TTTGCCACTCACTTTTCAATGAGTGAATTTGCAATGAGTGAATTTGCAATGAGTGAATTTCA 2409
 Qy
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 Db
 2410 AAGAAAATGCTGGGATGAGCAATTTTCAATGAGTGAATTTGCAATGAGTGAATTTCAATG 2469
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 2470 AAGCTAACTATGCTTTTAAAGGTTTCAAGGTTTCAAGGTTTCAAGGTTTCAAGGTTTCAAT 2529
 Db
 2470 AAGCTAACTATGCTTTTAAAGGTTTCAAGGTTTCAAGGTTTCAAGGTTTCAAGGTTTCAAT 2529
 Qy
 2530 GTTCTGAAATTTGCAAAATTTTCCACCGAGTTTCCACCGAGTTTCCACCGAGTTTCCACCG 2589
 Db
 2530 GTTCTGAAATTTGCAAAATTTTCCACCGAGTTTCCACCGAGTTTCCACCGAGTTTCCACCG 2589
 Qy
 2590 GAGTTGAGGATTTCTCTCTATTTGCCATTAATTTCCAAATGACATTTAAAGAGGAGCTTCA 2649
 Db
 2590 GAGTTGAGGATTTCTCTCTATTTGCCATTAATTTCCAAATGACATTTAAAGAGGAGCTTCA 2649
 Qy
 2650 AAACGGAAGAGAGAAATTTGACCGCATGCTGCTAGAGGTAATTTGACCGCATGCTGCTAGAG 2709
 Db
 2650 AAACGGAAGAGAGAAATTTGACCGCATGCTGCTAGAGGTAATTTGACCGCATGCTGCTAGAG 2709
 Qy
 2710 TTCTTACAGGATTTGCTGCTAGTTGCCATGATTAAGATGGAATTTCCAAAGCTGCTGAGG 2769
 Db
 2710 TTCTTACAGGATTTGCTGCTAGTTGCCATGATTAAGATGGAATTTCCAAAGCTGCTGAGG 2769
 Qy
 2770 AAGTTGAGGAAATGAAACCGACCTGAGAGGATGAGTTGACTCTCTGCTGCTGCTGCTG 2829
 Db
 2770 AAGTTGAGGAAATGAAACCGACCTGAGAGGATGAGTTGACTCTCTGCTGCTGCTGCTG 2829
 Qy
 2830 CAATTTCTTTTAAATTTCTTCAATTTAGAACTATCTTCTATTTCTGTAAGCTTTGGGGG 2889
 Db
 2830 CAATTTCTTTTAAATTTCTTCAATTTAGAACTATCTTCTATTTCTGTAAGCTTTGGGGG 2889
 Qy
 2890 GATACCTATGAGTTTGTGATATACTAGCTTATCTGTAAGCTTTGTAAGCTTTGTAAGCTTT 2949
 Db
 2890 GATACCTATGAGTTTGTGATATACTAGCTTATCTGTAAGCTTTGTAAGCTTTGTAAGCTTT 2949
 Qy
 2950 ACCCCAAACATGATTTCTGTAATCAGGGGACTTTTGTATGCTATTTCTGTTTAAATAGTAA 3009
 Db
 2950 ACCCCAAACATGATTTCTGTAATCAGGGGACTTTTGTATGCTATTTCTGTTTAAATAGTAA 3009
 Qy
 3010 GCGTTATCTTATATGTTCAAAAAA 3033
 Db
 3010 GCGTTATCTTATATGTTCAAAAAA 3033

RESULT 3
 US-10-425-114-31788
 ; Sequence 31788, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 31788
LENGTH: 2841
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: UC-ZMFLB73219B02_FLI
US-10-425-114-31788

Query Match 40.6%; Score 1231; DB 12; Length 2841;
Best Local Similarity 68.0%; Pred. No. 0;
Matches 1762; Conservative 0; Mismatches 820; Indels 9; Gaps 3;

QY	261	TGTTAGTGTGAGTAAACATGTTTGAACAATAGCTCTGACATCTCTTGGAGAGAT	320
DB	1	TGCCAGCGTGAGCAAGGCTATGTTGAGACCATTGCCCGCAACATTTTGTGGAAAGGAC	60
QY	321	GGACCGTACTCTTGAACTATATGAGGCGAGTGGTTCARACTGGAGCTGGTAAAGTGG	380
DB	61	TGACTGTGATTTGGAACTCTATGAGGGAAGTGGGTCAAAATGGAGGTTAACAAAGTCGG	120
QY	381	AACCCAGGGAATCTTGAAGATTTTGAAGATATCTGTGTCTTAATAATGAATGCMAAA	440
DB	121	AACACTGGAATATTTGGTAGTTTGAAGACATCTGTTTGCMAAATGACATGGAAGA	180
QY	441	TTCTCGGTGATGCTGCTCTTCTGCTCCAACTTCGGTCAAGATGGAATGGGCTT	500
DB	181	TTCCACAGTGATTTGTCTTCTTTCACGCGTCCGGAAGTCACTGTATGTAGGGCT	240
QY	501	AGGCTATGTTGATATTAACAGAGAGTCTCTGGTTTAAACAGAAATTTCTAGATGATGCA	560
DB	241	TAGTTTTTGGATATGACCAATAGGAGCTTGGGTTGGCTGATTTCCCGAAGATAGCGG	300
QY	561	CTTCAAAATTTGGAGTCTGCTTGGTCTCTTGGTTGACAGAAATGCTTTGACACGC	620
DB	301	ATTCACTAATGTTGAATCAGCTCTTGTGCAATAGGTTGCAAGGAGTGTCTTCCAGC	360
QY	621	GGAGACTGCAAAATCCAGTGAATAACGGCTATGTTTGAATGCAATATCTAGATGCGGCT	680
DB	361	AGATTGTGAAAAATCCATTTGACCTAAACCCCTTCAAGACGCTCATTTAGTAACTGT	420
QY	681	GATGTGTAAGTGAAGAAAGAACTGAATTTAAAGGAGAGATTTGGTACAGGATCTTGG	740
DB	421	TCGTGTGATGAGAAAGAAAGAGCTGACTTCAATCCAGGATCTCGCAAGATCTTGG	480
QY	741	TAGGCTCGTCAAGGGTTCAGTGAACCTGTTCGAGATTTGGTCTCTGGGTTGGAATGTC	800
DB	481	TAGAATAATCAGGGTTCTGTTGAGCCTGTACGTGATCTACTATCTCAGTTTGACTATG	540
QY	801	ATCAGCGCTTGGGGTGCAATCTTCTTAATGAGAACTACTTTCGGATGAGAGCAACTA	860
DB	541	TCCTGTCCTCCCTTGGAGCTCTTTATCTTATGTCGAGTTGCTAGCAGATGACATACTA	600
QY	861	TGGAATATACAGTCAACATACAACTCAATAGTTACATGATGATTTCTGCTGC	920
DB	601	TGGAATATACAGTCAACATACAACTCAATAGTTACATGATGATTTCTGCTGC	660
QY	921	TATGAGACACTGAATGTTATGAGAGCAAACTCAGATGCTTAATAAAAATTTTAGCTGTT	980
DB	661	AGTTCCAGCATTAACATTTCCAGAGGGAAGAACTGATGTAACAGAACTTCAGTTGTT	720
QY	981	CGTCTGATGAATAGAACGTTGCTGCTGGAATGGGTAAAGGTTATGCAATGTGGCT	1040
DB	721	TGGTTTGATGAACAGAACTTGTACTCTTGGATGGGAAAAAGATTCGTGAACAGATGGCT	780

QY	1041	GAAGCAACCTTTACTAGATGTAGAGAGATTAACTGTAGGCTGGATTTAGTTCAATCATT	1100
DB	781	GAACAACCTCTATTAGATGTTAATGAATTAATACCGACTAGACATGGTTTCAGGCTTT	840
QY	1101	CCTGAGGATGCTGGCTTTCGCCAAGATTGAGGCGAGATCTGAAAGAAATTTTCAGATAT	1160
DB	841	TGTAGAAGACCCCAACTCTGTCAGGACTCGGCAACAACTTAAGAGATTCAGATAT	900
QY	1161	TGAGCGCTGACACACAATCTTTGAGAGAAAAGACCCAGTTTGTGCACTGTTGTAATCT	1220
DB	901	TGATCTCTAAACACATAGTCTCCGAAAGAAATCACTAATCTGCAGCCTGTTGTTAAGCT	960
QY	1221	CTATCAGTCAAGTACAGAGTACCATATATCAAAAGTGTGTTGGAACGTCAATGAGGCA	1280
DB	961	TTATCAGTCTGTAGCAGAAATCCCATACATCAAGGCAATCTTCAGCAATATAATGGCCA	1020
QY	1281	ATTTGCAACACTCATCAGGGAAGGTATATTGATTTCTCTAGAGAAATGAGTGATGATAA	1340
DB	1021	ATTTTCACATTTGATAGGTCAAGTCTTCTGAAACGTTAGAGAAATGATGGCAAGAA	1080
QY	1341	TCACCTGAATTAAGTTCAATAGGCTCTTGTGAAACTTCTGTTGACCTTGATCAACTGAGAA	1400
DB	1081	TGGATTTGGTCTGGTTTCTTCTTGTGAGACAGCTATTGATCTTCTCAGCTGGAGAA	1140
QY	1401	TGGCAATACATGATTTCTTCTGCATATGACCCAAATTTATCTGCTCTCTGAAGATGACCA	1460
DB	1141	TGGAGAGTACAGAAATCTCTCTCTATATTTCTTCTGACTTGGGTGTTAAAGGATGAGCT	1200
QY	1461	AGAGACATTTGGAGCGACAAATTCATAATTTGACAAAACAACTGCCAATGATCTTGATCT	1520
DB	1201	TTCTGTGTTGAAACACCATATAACAACTGCACTGGATGATGATGATGATGATGATGATG	1260
QY	1521	AGCTATTGATTAAGTCACTTAAACTAGATAAGAAACAAATTTGGACAGCTCTTCAGAAAT	1580
DB	1261	TTCTCTTGAATAGCACTGAAGCTAGAAAAGGATCCCTCTTGGACATGTTGTTGAGAT	1317
QY	1581	TACCAAGAAAGAGAACCAAAAGTCCAGAGCAGCTAAATCTCTCACTACATTTGTTCTCA	1640
DB	1317	GTCAAGAAAGAGGAAACAGAAAGTCCAGAGAAACCTCACTGGCAGCTACTTAAATCATAG	1377
QY	1641	AACAGCTAAGGATGGGTAAAGTTCACTATACAAAACCTCAAAAACCTAGGAGATCAGTT	1700
DB	1378	AACTGTAAGATGTTGATTAAGTTCACAAACTTAAGCTGAAATCTAAGTGAATCAATA	1437
QY	1701	CCAGAAATGTTGAGAGAGTACAAAAGTGTCCAGAAAGAAATTTGGTAGCTGCTGATTTCA	1760
DB	1438	CCAGGCAATTTGTTGGTGAGTACACAAAGTTGTCCAGAAAAGGTTGGTGTGATGATGAG	1497
QY	1761	AACAGCTCGAGTTTCTCCGAGGCTTTGCGAGTATAGCTGGTGTACTTGTCTGAGTTGGA	1820
DB	1498	GGTTTCAGGCACTTCTCAGAGGTATTTGAAATTTTGTCTGAGTTCTGTCCGAGTTGGA	1557
QY	1821	TGTGTTACTGAGTTTTCGGGATTTGCGCTGCCAGTTTGCCTCACTCCCTACACAAGACCAA	1880
DB	1558	TGTTTTTCAAAAGTTTGTCTGATTTGCGCAACTAGTTTGCCTGCTTCTTATGTTAGGCCA	1617
QY	1881	TATCAGTCCACAGATACAGGAGATATTATCTTGAAGGTTGAGCATCTCTTGTGTGGA	1940
DB	1618	CATCACTCGGTCCGATGAAGGAGATTTGTTCTACTGGGTAGCAGACATCTTGTCTAGA	1677
QY	1941	AGCTCAAGATTTGGGTTAACTCCATTTCTTAAGCTAGTACTAGTTAGGGAGAGGTTG	2000
DB	1678	GGCAAGAAATGTTTAACTTTTATCCCAATGATTTGCACTCTGGTGAGGGGAAAGTTG	1737
QY	2001	GTTCAGATTTATCAGGCGCTTAAACATGCGGTGGAAGTCCAGCTACATTTCCGACAGTTGG	2060
DB	1738	GTTCAGATCATCACTGGACCAACATAGGAGGAAATCCCAATTTATAAGACAGGTTGG	1797
QY	2061	TGTGAATGCTGTGAGGCGCCAAAGTTGGCTGTTTGTCTTCAATGTGCAATGTCAATTTTC	2120
DB	1798	TGTAATGTTATGAGGCAAGTTGGTTCTTCTGACCTTGTGATCAAGCAAGCATTAG	1857
QY	2121	TATTCGTGATTTGTTTGTCTGCTGCTGGCCCTGGAGATTTGCCAGCTGAGAGGATTTTC	2180

1858	TGTGAGGATGTTATTTTCTCGTGTGGCGTGGTGATTCGCAACTCATGGTGATC	1917
2181	TACTTTTATGCAAGAGATGCTTGAGACTGCATCGATCTTTGAAGAGAGCTACTGATAGATC	2240
1918	AACCTTTATGCAAGAAATGCTTGAAACAGCATCCATCTAAAGAGCGCCTCTGATAAGTC	1977
2241	ATTGATTAATAATTGATGAGTTGGGCGCTGGGACATCAACCTACGATGGCTTTGGTTTAGC	2300
1978	TCCTATAAATTTATTGATGAGCTGGGGCGTGGAACTTCCACATATGATGGATTTGGTCTTGC	2037
2301	TTGGGCTATTTTGTGAGCACATTTGTGAAGAAAATTAAAGACCAACAACTGTTTGCCCACTCA	2360
2038	ATGGGCTATCTGTGAGCATCTTATGGAATGACTCGAGCGCCTACCTGTTTGGCAACCCA	2097
2361	CTTTCATGAGCTGACTGCATTAGC--CAACAAGAATGGAGACAATGGACATTAAGAAAAA	2417
2098	TTTCCATGAACCTAACTGATTAGCACATAGAAATGATGATGAGCACCAACACATTTTCAGA	2157
2418	TGCTGGATAGCAAAATTTTCATGTTTTCACACATGACCTCTTAATCGCAAGCTAAC	2477
2158	CATCGGAGTTGCAAAATTTATCACGTGGGTGCTCACATAGACCCATTAAGTAGGAAGTTAA	2217
2478	TATGCTTTTCAAGGTTCCACGAGTGCTTGATCAGAGTTTGGTATTCACTGTGCTGA	2537
2218	TATGCTTTTCAAGGTTGAACTGTTGATCGACACCAAGTTTGGTATTCACTGTGAGA	2277
2538	ATTTGGCAAAATTTCCACCGAGTGTGTGGCTCTGGCTAGAGAAAAGGCATCTGAGTTGGA	2597
2278	ATTTGTCTAAATTTCCAGAAGCTGTTGTGGCCCTTGGGAAAAGCAAGCAGCAGAGTTAGA	2337
2598	GGATTTCTCTCCATATGCCATAATTCCAAATGACATTAAA--GAGCGAGCTTCAAAACG	2654
2338	AGACTTTTCTACTACACTACCTTTTCGATGATTTGAAGACAGAGTTGGATCAAGCG	2397
2655	GAAGAGAGAAATTTGACGCCCATGACGTGCTAGAGGTACTGCCAGAGCTCGGCAATTCCT	2714
2398	CAAGAGGGTATTAGCCCCAGATGACATCACGAGAGGAGCTGCACGGGCTCGGCTTTTCT	2457
2715	ACAGGATTTGCTCAGTTGGCACTGGATAGATGGATTCAAAACGTGGTAGGCAAAAGTT	2774
2458	TGAGGAATTCGCGCATTTGCCATTATGGAATGAGATGGATGGGAGCAAGATCTTGGAGATGGC	2517
2775	GAGCAAAATGAAAACCGACTGGAGAGGGATGCAGTTGACTCTCACTGGCTTCAGACAAAT	2834
2518	CACCAAGATGAAAGCTGACTGTGCAAGAAGATGCAGCTGACAATCTTGGCTCCAGAGTT	2577
2835	CTTTTAATTTCT	2845
2578	CTTCTGAAGCT	2588

RESULT 4
 US-10-424-599-71262
 ; Sequence 71262, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 71262
 ; LENGTH: 2151
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT MRT3847 35361C.1

US-10-424-599-71262
 Query Match 35.1%; Score 1063.2; DB 12; Length 2151;
 Best Local Similarity 75.6%; Pred. No. 2e-287;
 Matches 1346; Conservative 0; Mismatches 428; Indels 6; Gaps 2;

QY	1069	ATTAACTGTAGGCTGATTTAGTTTCAATCATTCGTGGAGGATGCTCGCTTCCCAAGAT	1128
DB	1	ATTAAATTCCAGGTTGGACATAGTTTCAAGCATTTGTAGAGGACATCTGCTTTCGCCAAGAT	60
QY	1129	TTGAGCGAGCATCTGAAAAGAAATTTTCAGATATTTGAGCGGTGACACACAAATCTTGAGAGG	1188
DB	61	CTGAGCGAGCATCTGAAAAGAAATATCAGACATTTGAGCGATTTGATGCACAATATTCAGAAG	120
QY	1189	AAAAGAGCCAGTTTATGTGACAGTTTGTAAAACCTTATCATCAGTCAAGTACAGAGTACCAAT	1248
DB	121	CGAGGAGCTGGTCTGCAACATATTTGTTAAACTTTATCAGTCAAGTATTAAGTACCTTAC	180
QY	1249	ATCAAAAGTGTTTTGGAAAGCTCATGATGGCAATTTTGCACACATCTATCAGGGAAGGTAT	1308
DB	181	ATCAAAAGTGTCTTGGAAAGATATGATGGACAATTTTCCAATGATGAGGAGTAGGTAT	240
QY	1309	ATTGATTCTCTAGAGAAATGCGAGTGATGATAATCACTCGAATAAGTTTCATAGGTTCTTG	1368
DB	241	CTGGAACCTATTGAGTTATGGACTGATGATGAGCAGCTGACAAAATTCATGGGCTTGTA	300
QY	1369	GAACCTTCTGTGACCTTGATCAACTGTGAAATGGAAGATPACATGATTTCTTCTGCATAT	1428
DB	301	GAAGCTTCTGTTGACCTTGATCAACTGGGAAATAGGGAATACATGATTTCTCCAAGCTAT	360
QY	1429	GACCCAAATTATCTGCTCTGAAGGATGAGCAGAGACATTTGGAGGCGACAAATTCATAAT	1488
DB	361	GACTCTATATAGCTAACCTTAAAGGACCAACAAGAATTTCTAGAGAGCCAAATACAAAC	420
QY	1489	TTGCACAAAACAACTGCGCAATGATCTTGATCTACCTATTGATAAGTCACCTTAAACTAGAT	1548
DB	421	TTGCATAGACAAACTGCTGATGATCTTGATCTGCTATGACCAAGGCAATTAAGTTAGAC	480
QY	1549	AAAGAAACACAAATTTGGACACGCTCTTCAGAAATTAACAAGAAAGAAACAAAGTCAGG	1608
DB	481	AAGGCACACAAATTTGGACATGTTTTCAGAAATCACAAGAAAGGAGGACCAAAATAAGG	540
QY	1609	AAGAGCTAAATCTCATCTACATTTGTTCTCGAAACACGTTAAGGATGGGTAAAGTTCAAC	1668
DB	541	AAGAAGCTCAATCTCATGTTTATTTATCTGGAAACCCGTTAAGATGGAGTGAAATTTACC	600
QY	1669	TATACAAAACCTCAAAAACCTAGAGAGTACGTTCCAGAAGATTTGTAGAGGAGTACAAAAGC	1728
DB	601	AACAGAGCTCAAGAAACTAGGGAGCCATATTCACAAATTTCTTGGAGGATATAAAGT	660
QY	1729	TGTTCAGAAAGAAATGGTGTAGTTCGTGTAGTTTCAAAACAGCTCGAGTTTCTCCGAGGTGTTT	1788
DB	661	TGTCAAAAAGGTTAGTTGATAGAGTAGTTTCAAACTGCGGCAACTTCTCTGAGGTGTTT	720
QY	1789	GCAGGTATAGCTGGTGTACTTGTCTGAGTTGGATGTGTACTGTAGTTTTCGGGATTTGGCT	1848
DB	721	GAATCTTTAGCTCAAAATAAATTTCTGAAATTTGGATGTATTTACTGAGCTTTGCTGATTTGGCT	780
QY	1849	GCCAGTTGGCCCAACTCCCTACACAAGACCAAAATATCAGTCCACAGATACAGAGATATT	1908
DB	781	TCATGTTGCTTACTCCCTACACAAGCCCTGACATCATCTTCATCGGACGAGGAGATATT	840
QY	1909	ATATCTGAAGGGGTGATGGCATCTTGTGTGAAAGCTCAAGATTTGGGTTAACTCCATTCCT	1968
DB	841	ACTTTAGAAGGATGCAGACACCCCTTGTGTAGAGGCAACAAGCTGGGTGAATTTTATACCA	900
QY	1969	AATGACTGTAGACTAGTTAGGGAGAGAGTTGGTTTCAGATTATACAGGCCCTTAACATG	2028
DB	901	AATGATTTGTAAGCTTTGTTCAGAGGAAAACTTTGGTTTCAATAATAACAGGACCTTAACATG	960
QY	2029	GGTGGAAAGTCGACTACATTTCCGACGGTTGGTGTGAATCTCTGATGGCCCAAGTTGGC	2088
DB	961	GGTGGGAAATCAACATTTATCCGACAGGTGGGTGTTAAATATTTTGTATGGCAAGATTGGT	1020


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Qy 2089 TCGTTTGTTCATGTGCAATGCTACCATTTCTATTCTGTGATTCATTTTGTCTGTGTT 2148
Db 1021 TCCTTGTGTTCTGTGCAATGCCAGCATATCTGTCCGTGATGCAATTTTGGCCGCTGT 1080
Qy 2149 GGGCTCGAGATGCCAGCTGAGAGGATTTCTACTTTTATGCAAGAGATGCTTTGAGACT 2208
Db 1081 GGTGCTGTGACTGTCAACTTCGTGGAGTTTCTACCTTTATGCAAGAAATGCTTTGAAACT 1140
Qy 2209 GCATGATCTTGAAGAGGACTACTGATAGATCATTTGATTAATGATGATGATGGCGGT 2268
Db 1141 GCATCAATATTAAGAGGAGCTACTGACAAAGTCCTTGATTAATCATTTGATGATGGGACGT 1200
Qy 2269 GGGACATCAACTACGATGCTTTGTTTGTGTTTGTGTTTGTGTTTGTGACCATTTGTTGAA 2328
Db 1201 GGGACATCAACTATGATGATGTTTGTGTTTGTGTTTGTGTTTGTGACCATTTGTTGAA 1260
Qy 2329 GAAATTAAGACCAACATTTGTTGCCACTCATTTTCAATGAGCTGACTGCAATTAAGCCAAAC 2388
Db 1261 GTAATCAAGCACCTACTTTGTTGCCACCTTTTCAAGAAATGACTGCAATTAAGCCCTT 1320
Qy 2389 AAGNATGGAGCAATG--GACATAAGAAATGCTGGGATAGCAAAATTTTCAATGTTT 2445
Db 1321 GAAATGTAAGCAATGATTCACAGAAGCAAAATTTGTTGGTGGCAAACTATCATGTTAGT 1380
Qy 2446 GCACATTTGACCTTCTAATCGCAAGCTAACTATGCTTTTACAAAGTTTCACCCAGGTGCT 2505
Db 1381 GCATATTTGACTCATCACTCGAAGCAATCAACATGCTATACAAAGTTTGAACCTGGAGCT 1440
Qy 2506 TGTGATCAGAGTTTGGTATTCATGTTGCTGAAATTTGCAAAATTTTCCACCGAGTTTGTG 2565
Db 1441 TGTGATCAGAGTTTGGTATTCATGTTGCTGAAATTTTGCAGATTTCCCTGAAAGTTTGT 1500
Qy 2566 GCTGCTGATAGAAAGGATCTGAGTTGAGAGATTTCTCTCTATTTGCCATTAATTCCTCA 2625
Db 1501 ACCATGCTAGAGAAAGGCGAGCAATTTAGAAGACTTTTCTCTTCTGCAACATCCTTA 1560
Qy 2626 AATGACATTA--AAGAGGAGCTTCAAAAGGAGAGAGATTTGACCGCATGAGCTG 2682
Db 1561 AATCTACTACAGAGGAGTGGTTCTTAACGTAAGAGAGCATTTGAACCGATGACATG 1620
Qy 2683 TCTAGAGTACTGCCAGCTCGGCAATTTCTACAGGATTTTCGCTCAGTTTGCCACTGGAT 2742
Db 1621 TCTCAAGGGCTGCAAGGCTCGCAATTTCTAGAAGCATTTGTTGCTTTGCCCTTAGAA 1680
Qy 2743 AAGATGATCAACAGTGTGTCAGGCAAAAGTTGAGCAAAATGAAACCGACTGGAGG 2802
Db 1681 ACCATGACAAATGCAAGCTTTGCAAGAGTAAAGAGTTTAAAGATATCTTTGGAGAAG 1740
Qy 2803 GATGAGTGTGACTCTGCTGCTTTCAGCAATTTCTTTTAAAT 2842
Db 1741 GATGCAAAACTGTAATTTGGCTGCAACAGTTCTTTAGT 1780

```

RESULT 5
 US-10-425-114-12569
 ; Sequence 12569, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(5313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 12569
 ; LENGTH: 1964

```

; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 701182994_FLI
; US-10-425-114-12569

Query Match      27.2%  Score 825;  DB 12;  Length 1964;
Best Local Similarity 68.8%  Pred. No. 1.7e-220;
Matches 1179;  Conservative 0;  Mismatches 525;  Indels 9;  Gaps 3;

Qy 1139 ATCTGAAAGAAATTCAGATATTGAGCGGTGACACACAATTTCTTGGAGGAGAAAGAGCCA 1198
Db 1 AACTTAAAGAAATATCAGATATTGATCGTCTAAACACATAGTCTCCGAAGAAATCAGCTA 60
Qy 1199 GTTTAGTGCAAGTTTAAAACTCTATCAGTCAAGTACAGAGTACCATATATCAAAAGTG 1258
Db 61 ATCTGCAAGCTGTTTAAAGCTTTATCAGTCTCTGTAGCAGAAATCCATATCATCAAGGCA 120
Qy 1259 TTTTGGAAACGTCAATGATGGGCAATTTGCAACACATCATCAGGAAAGGTATATTGATTCTC 1318
Db 121 TTCTTCAAGCAATATATAGGCAATTTTCAACATTTGATAGGTCAAGTTTCTTGAACGGT 180
Qy 1319 TAGAGAAATCGAGTGAATGATTAATCACTGAATAGTTTATAGTCTTTGTGAAACTTTCTG 1378
Db 181 TAGAAGAAATCGATGGCAAGAAATCGAATTCGTCGTTTCTCTCTTCTTGTGAGACAGCTA 240
Qy 1379 TTGACCTTGAATCAACTTGAGAAATGAGAAATACATGATTTCTTCTGCAATGACCAAAAT 1438
Db 241 TTGATCTTGTCTGAGTGGAGAAATGAGAGATACAGAAATATCTCTCTATATTTCTTCTGACT 300
Qy 1439 TATCTGCTCTGAAAGATGAGCAAGAGACATTTGGAGCGACAAATTCATAATTTGCACAAAC 1498
Db 301 TGGGTGTAATTAAGGATGAGCTTTCTGTGTTGAAACCAATTAACAAATCTGCACGTTG 360
Qy 1499 AAATGCAATGATCTTTGATCTACCTATTGATAGTCACTTAAACTAGATAAGAAACAC 1558
Db 361 ATACAGCTAGTATCTGATCTTCTGTTCTGTAAGCACTGAGCTAGAGAAAGAGATCCC 420
Qy 1559 AATTTGACACAGCTTTCAGAAATTAACAAGAAAGAAACCAAAAGTCAAGNAGCAGCTAA 1618
Db 421 ---TTGACATGTTTTCAGAAATGTCAAAGAAAGAGGAAACAGAAAGTCAAGGAAACCTCA 477
Qy 1619 ATTCTCACTACATTTCTCGAAACAGTAAAGATGGGTAAAGTTTCACTTATACAAAC 1678
Db 478 CTGGCAGCTACTTAATCATAGAAACTCTGTAAGATGTTGTAAGTTTCAAAATTTCTAAGC 537
Qy 1679 TCAAAAACCTAGGAGATCAGTTTCCAGAAAGTTTGTAGAGGAGTACAAAGCTGTGAGAAAG 1738
Db 538 TGAATAATCTAAGTATCAATACCAGGCAATTTGTTGGTGAAGTACACAAATTTGTGAGAAA 597
Qy 1739 AATTTGATGCTGTGATTTCAAAACAGCTCGGAGTTTCTCGAGGTTTTCAGGATATAG 1798
Db 598 AGGTGTTGTTGATGATGAGGTTTTCAGGCAATTTCTCAGAGGATATTTGAAATTTTG 657
Qy 1799 CTGGTGTACTTGTGATGTTGATGTTTCTGAGTTTTCGGGATTTTGGCTGCCAGTTTGGC 1858
Db 658 CTGAGTTTCTGTGGAGTTGATGTTTCAAAAGTTTTCGTTGTTGTTGTTGCAACTAGTTGCC 717
Qy 1859 CAACTCCCTACACAAGACCAAAATATCAGTCCACAGATACAGGAGATATTAATCTTGAAG 1918
Db 718 CAGTTCTTATGTTAGGCCAGACATCACTGCGTGGATGAAGGAGATATTTGTTCTACTGG 777
Qy 1919 GGTGTAGGATCTTGTGTTGTTGAGAGCTCAAGATTTGGTTAACTCCATTCCTTAAGTACTGTA 1978
Db 778 GTAGCAGACATCTCTGTTGTAGAGGCAACAGATGTTTAACTTTTATACCAATGATTTGCA 837
Qy 1979 GATTAGTTAGGGAGAGAGTTGTTTTCAGATTAATCAAGCCCTTCAACATGGGTGGAAGT 2038
Db 838 CTCTGTTGAGAGGAGAAAGTTGGTTTTCAGATCATCTGAGCCAAACATGGGAGGAAT 897
Qy 2039 CGACCTACATTCGGCAGAGTTGTTGTTGAAATCTCTGATGGCCCAAGTTGGCTCGTTTGTTC 2098
Db 898 CCACATTTATAAGACAGGTTTGGTTGTAATGTTTATTTGATGGCAAGTTGTTCTTCTTCTAC 957

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QY 2099 CATGTGCAATGCTACCAATTTCTATTCTGTGATGTATTTTCTGCTGTTTGGCGCTGGAG 2158
Db 958 CTTGTGATCAAGCAAGTATGTAGTGTGAGGATGTATTTTCTGCTGTTTGGCGCTGGTG 1017
QY 2159 ATTGCGAGCTGAGAGGAGTTTCTACTTTTATGCAAGAGATGCTTGAGACTGCATCGATCT 2218
Db 1018 ATTGCGAACTTCATGGTGATCACTTTTATGCAAGAAATGCTTGAACAGATCCATCC 1077
QY 2219 TGAAGGAGCTACTGATAGATCATTTGATTAATTAATGATGTTGGCGCTGGGACATCAA 2278
Db 1078 TAAAGGCGCTCTGATAAGTCTCTTATAATTAATGATGAGTGGGCGTGGAACTTCCA 1137
QY 2279 CTTAGATGGCTTTGGTTAGCTTGGGCTATTTGAGACACATTTGTTGAAGAAATTAAG 2338
Db 1138 CATATGATGGAATTTGGCTTTCATGGGCTATCTGTGAGCATCTTATGGAAGTGAATCGAG 1197
QY 2339 CACCAACATTTGTTGCCACTCACTTTCAAGAGCTGACTGCAATGAC---CAACAGAAATG 2395
Db 1198 CGCTACCTTGTGCAACCCATTTCCATGAATTAATGCAATGCAATAGAAATGATG 1257
QY 2396 GAGCAATGSGACATGAAGAAATGCTGGATAGCAAAATTTTCATGTTTTCACACATTTG 2455
Db 1258 ATGAGCAACCAACATTTTCAGACATCGGAGTTGCAAAATTTATCAGTGGTGTCTCACATAG 1317
QY 2456 ACCCTTCTAATCGCAAGCTAATGCTTTTACAGGTTTCAACGAGTGTGTTGCTCTGGCTA 2515
Db 1318 ACCCAATTAAGTAGGAAGTAACTATGCTTTTCAAGGTTTGAACCTGGTGCATGCGACCAA 1377
QY 2516 GTTTTGTATTCATGTTGCTGATGTTGCAAAATTTTCCACCGAGTGTGTTGCTCTGGCTA 2575
Db 1378 GTTTTGTATTCATGTTGCAAGTGTGTAATTTTCCAGAGCTGTGTTGCTCTGGCTA 1437
QY 2576 GAGAAAGGATCTGAGTTGAGGATTTCTCTCTATTTGCCAATTTCCAAATGACATTA 2635
Db 1438 AAAGCAAGCAGCAGGTTAGAGACTTTTCTACTACACTTCTTCCGATGATTTGA 1497
QY 2636 AA---GAGCGAGCTTCAAAACGAGAGAGATTTTGAACCGCATGACGTGTAGAGTA 2692
Db 1498 AAGCAGAGTTGGATCAAGCGCAGAGGATTTTATGCCCCAGATGACATCACCAGAGAG 1557
QY 2693 CTGCGAGAGCTCGGCAATTTCTACAGGATTTTGGCTCAGTTGCGCACTGGATGAAGTGA 2752
Db 1558 CTGCGAGGCTCGGCTTTTCTTGGGAATTCGCGCAATTCCTATGATGAGATGATG 1617
QY 2753 CAAGCTGCTCAGGCAAAAGTTGAGCAAAATGAAACCGCACTGAGAGGAGTGCAGTTG 2812
Db 1618 GGAGCAAGATATTGGAGATGGCCACCAAGATGAAAGCTGACTTGCAGAAAGATGCAAGCTG 1677
QY 2813 ACTCTCACTGGCTCAGCAATTTCTTTAATTTCT 2845
Db 1678 ACAAFTCTGGCTCAGCAGTTCTTCTGAAGCT 1710

```

RESULT 6
US-10-425-114-3918
; Sequence 3918, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 3918
; LENGTH: 1723

```

; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700344029_FLI
US-10-425-114-3918

Query Match      23.3%; Score 706.4; DB 12; Length 1723;
Best Local Similarity 66.8%; Pred. No. 3.3e-187;
Matches 1023; Conservative 0; Mismatches 58; Indels 3; Gaps 1;

QY 529 CTTGCTTTTAAACAGAAATTTCTAGATGATGAGCACATTCACAAATTTGGAGTCTGCTTTGTT 588
Db 3 CTTGGTTGGCTGAGTTTCCGAAGATAGCGGATTCATAATGTTGAATCAGCTCTGTT 62
QY 589 GCTCTTGGTTGACAGAAATGTCTTTGTACCAAGCGGAGCTGSCAAATCCAGTGAATACAGG 648
Db 63 GCATTAGGTTGCAAGGAGTGTCTTCTCCAGCAGATGTGAAAAATCCATTGACTTAAT 122
QY 649 CCTATGTTTGTGCAATATCTAGATGCGGCGTGTAACTGAAAGAAAGAACTGAA 708
Db 123 CCCCTTCAAGACGTCATTAGTAACTGTAATGTTCTGTGACTGAGAAAAAAGAGGCTGAC 182
QY 709 TTTAAAGGAGAGATTTGGTACAGGATCTTGGTAGGCTCGTCAAGGTTTCACTAGTAACT 768
Db 183 TTCAAATCCAGGATCTCGCACAGATCTTGGTAGAATATCAGGGTTCTGTTGAGCCT 242
QY 769 GTTCGAGATTTGGTCTCTGGGTTGCAATGTGCAATGAGCGCTTTGGGGTGCATCTTCT 828
Db 243 GTAGCTGATCTACTATCTCAGTTTGAATGCTATGCTCTTGTGCTGCTGAGCTCTTTTATCT 302
QY 829 TATGACAACTACTTGGGATGAGAGCAATCTGGAACACTATACAGTCAAACATACAC 888
Db 303 TATCCGAGTTGCTAGCAGATGACATACTATGGAATTTACAAATGGAAGTACAA 362
QY 889 CTCAATAGTTACATGAGATTAGATTCTGCTGCTATGAGAGCACTGAATGTTTATGAGAGC 948
Db 363 TTGAACCTGCTACATGCGACTTGTCTGCTGCACTTCGAGCATTTAAACATTTGCAAGGG 422
QY 949 AAATCAGATGCTAATAAAATTTTGTGCTTGTGCTGCTGATGATGAACTAGAACTGCTGCT 1008
Db 423 AAAGCTGATTAACAAGAACTTCAGTTGTTGTTGTTGTTGATGAACAGAACTTGTGCTGTT 482
QY 1009 GGAATGGGTAAGAGTTTATGCACTGCTGCTGAGCAACCTTTACTAGATGTTAGAGAG 1068
Db 483 GGGATGGGAAAGAGTTGCTGAACAGATGGCTGAAACAACTCTATTAGATGTTTAAATGAA 542
QY 1069 ATTAACCTGTAGGCTGGAATTTAGTTCAATCTTCGTGAGGATGCTGCGCTTCGCGCAAGAT 1128
Db 543 ATTAATACCGACTAGACATGGTTTCAGGCTTTTGTAGAAGACCCAGAACTTCGTCAGGGA 602
QY 1129 TTGAGGCGAGCATCTGAAAAGAAATTTTCAATATTTGAGCGGCTGACACAACTTTGAGAGG 1188
Db 603 CTCGGCAACAACTTAAAGGATATCAGATATTGATGCTCTAAACACATAGTCTCCGAAAG 662
QY 1189 AAAAGAGCCAGTTTGTAGTGCAGCTTTGTAATACTCTATCAGTCAAGTACCCAGAGTACCATAT 1248
Db 663 AATCAGCTAATCTGACGCTGTTGTTAAGCTTTATCAGTCTGCTGAGCAATCCCATAC 722
QY 1249 ATCAAAAGTGTTTTGGAACTGCTGATGAGGCAATTTTGCAACACTCATCAGGGAAGGTAT 1308
Db 723 ATCAAGGGCATTTCTCAGCAATATATATGCGCAATTTTCAACATTTGATAGGTCAAAGTTT 782
QY 1309 ATTGATTTCTTAGAAGAAATGAGTGAATGATTAATCACCCTGAAATGATTTTCAAGTCTTGTG 1368
Db 783 CTTGAACCGTTAGAAGAAATGATGGCAAGAAATCGAATTTGCTCGGTTTCTTCTCTGTT 842
QY 1369 GAAACTTCTGCTGACCTTGTATCACTTTGAGAAAGGAAATACATGATTTCTTCTGCAATAT 1428
Db 843 GAGACAGCTATTGATCTTGTCTGAGTGGAGATGGAGATGACAGAAATATCTCTCTATAT 902
QY 1429 GACCCAAATTTATCTGCTCTGAAGGATGAGCAAGAGACATTTGGAGCGACAAATTCATAAT 1488
Db 903 TCTTCTGACTTGGGTGATCTAAGGATGAGCTTCTGCTGTTGAAACCAACATTAACAT 962

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QY	1489	TTGCACAAACAAACTGCGCAATGATCTTGTACTCTACCTATTGATAGTGCACCTTAAACTAGAT	1548
Db	963	CTGCACGTGGATACAGCTAGTGTCTGGATCTTCTGTTGATAAGCAACTGAAGCTAGAA	1022
QY	1549	AAAGAAACACAAATTTGGACACGCTTTCAGAAATTACCAAGAAAGACCAAAAGTCAGG	1608
Db	1023	AAAGGATCCC---TTGGACATGTGTTTCAGAAATGTCAAAGAAAGAGGACACAAAGTCAGG	1079
QY	1609	AAGCAGCTAAATCTCACTACATTTGTTCTCGAAACACGTAAGCATGGGTAAAGTTTCACC	1668
Db	1080	AGAAGACTCACTGGCAGCTACTTAATCATAGAAACTCGTAAAGATGGTAAAGTTTCACA	1139
QY	1669	TATACAAAACCTCAAAAACCTAGGAGATCAGTTCACAGAAAGTTGTAGAGGAGTACAAAAGC	1728
Db	1140	AAATCTAAGCTGAAAAAATCTAAGTGATCAATACCAAGSCAATGTTTGGTGAGTACACAAGT	1199
QY	1729	TGTCAGAAAGAAATTTGGTAGTCTGTGTAGTTTCAACACAGCTCGAGTTTCTCCGAGTGGTTT	1788
Db	1200	TGTTCAGAAAAGGTGGTTGGTGATGTAGTCAGGGTTTTCAGGSCACATCTCCAGAGGTATTT	1259
QY	1789	GCAGGTATAGCTGGTGTACTTGCTGAGTTGGATGTGTTACTGAGTTTTCGGGATTTGGCT	1848
Db	1260	GAAAAATTTTGCTCGAGTCTGTGCGAGTTGGATGTTTACAAAGTTTTCGTGATTTGGCA	1319
QY	1849	GCAGTTGCCCAACTCCCTACACAGACCAAAATATCAGTCCACAGATACAGAGATATT	1908
Db	1320	ACTAGTTGCCAGTTCCTTATGTTAGGCCAGACATCATCTCGTCGGATGAAGGAGATATT	1379
QY	1909	ATACTTTGAAGGGGTGATGGCATCTCTGTGTGCGAAGCTCAAGATTGGGTAACTCCATTCCCT	1968
Db	1380	GTTTCTACTGGTAGCAGACATCTTGTCTAGAGGCACAGATGGTGTTAATTTATACCC	1439
QY	1969	AATGACTGTAGACTAGTTAGGGAGAGAGTTGGTTTCAGATTATCAAGGCCCTTAACATG	2028
Db	1440	AATGATTGCACCTCTGGTGAGAGGAAAAAGTTGGTTTCAGATCATCATCTGGACCAACATG	1499
QY	2029	GGTGGAAAGTCGACTACATCTCGCAGGTGG	2060
Db	1500	GGAGGAAAATCCACATTTATAAGACAGGTTAG	1531

```

RESULT 7
US-10-270-839-48
; Sequence 48, Application US/10270839
; Publication No. US20030143586A1
; GENERAL INFORMATION:
; APPLICANT: Chao, Qimin
; APPLICANT: Grasso, Luigi
; APPLICANT: Sass, Philip M.
; APPLICANT: Nicolaides, Nicholas C.
; TITLE OF INVENTION: Genetic Hypermutable of Plants for Gene Discovery and Diagnosis
; FILE REFERENCE: AG0002US (MOR-0133)
; CURRENT APPLICATION NUMBER: US/10/270,839
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/328,750
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 5307
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-10-270-839-48

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	Query Match	22.6%	Score 685.8	DB 14	Length 5307
	Best Local Similarity	63.4%	Pred. No. 4.4e-181		
	Matches 1149	Conservative	0	Mismatches 522	Indels 140
					Gaps 1
QY	126	TAGGGCAGTTTCGGCTCTTTGATCGTCGGGACTATTATACATCTCATCGGATGATGCAAC	185		
Db	1096	TATGGAAATTTTITGAATGCATTTTCGAGGATTTATACAGCTCATGGTGAAATTCAGT	1155		

QY	186	TTTCA	TTGCAGAGACATATTTACACACACAACTGCGGTATACGACAGTTGGGTAAATAGAGC	245
Db	1156	TTTCA	TTGCAAAAGACTTATTTATCATCAACCACTGCTACGTCAGCTCGGGAGTGGTTC	1215
QY	246	TGATG	CCCTTTCCAGTGTGTAGTGTGAGTGAACATGTTTGAACAAATAGCTCGTGACAT	305
Db	1216	AAATG	CTTTTCAAGCGTAAAGCAATTAGTAGGAACATGTTTCAAAACGATTTGCTTAGGATCT	1275
QY	306	TCCTT	GGAGAGAAATGGACCGTACTCTTGAACATATATGAGGGCAGTGGTTCAAACCTGGAG	365
Db	1276	TCCTC	GGAGCGTAATGATCATACTCTAGAACCTTTATGAAGGAAGCGGATCGAATTTGGAG	1335
QY	366	ACTGG	TAAAAAGTGAACCCAGGGAATCTTTGGAAGTTTGGAGGATATCTCTGTTTGGTAA	425
Db	1336	ACTTG	TGAACAACAGGTTCTCTCGAACAATGGAAGCTTTGAAGATGTTTGTGTTGCAAA	1395
QY	426	TAATG	AAATGCAAAATTCCTCGGTGATGTGCTCTTGCTTCCAAACTTCGGTCAGAATGG	485
Db	1396	CAATG	AAATGCGAGACACACCAGTTGTTGTCCTCATATTTCCAAGTTTTCACGATGGCAG	1455
QY	486	ATGTG	AAGTTGGCTTAGGCTATGTTGATATTAATAAGAGAGTCCCTTGGTTTAAACAGAATT	545
Db	1456	ATCGT	TATTTGGGATGGCCTATGTTGATCTGACTAGGCGAGTTCTTTGGACTAGCTAGATT	1515
QY	546	TCTAG	ATGATAGCCTTCAAAAATTTGGAGTCTGCTTGGTTGCTCTTGGTTGCGAGAGA	605
Db	1516	TCTTG	ATGATAGCCGCTTCAACCAATCTGGAGTCTTCGTTGATTTGCTCTAGGGCCAAAAGA	1575
QY	606	ATGCT	TGTACAGCGAGACTCGCAAACTCCAGTGAATACAGGCTTATGTTTCATGCAAT	665
Db	1576	ATGCA	TTTTTCCAGCTGAATCCGCAAAATCCAATGAATGCAAAAGCTGTATGATTCCT	1635
QY	666	ATCTA	GATGGCGTGATGGTTAACTGAAGAAAGAAAACCTGAAATTTAAAGGGAGAGATTT	725
Db	1636	GGAGG	GTGTGCGTGATGATTAACAGAGAGGAAGAAACACGAGTTCCAAAGGAAGAGATTT	1695
QY	726	GGTAC	GAGATCTTTGGTAGGCTGTGTAAGGGTTCAGTAGAACCTGTTGCGAGATTTGGTCTC	785
Db	1696	AGATT	CAGATCTTTAAGAGATTTGGTGAAGGGGAATATTAGCCCTGTTAGAGATTTGGTATC	1755
QY	786	TGGTT	TCGAATGTCATCAGGCGCTTTGGGGTGCATCTTCTTATGCGAACCTACTTGC	845
Db	1756	CGGTT	TGACCTTGGCACTCCTGCTCTAGTGCAATTACTCTCGTTTCTGAACTTCTCTC	1815
QY	846	GGATG	AGACAACTATGGAACCTATACAGTCAAAACAATAACAACCTCAATAGTTTACATGAG	905
Db	1816	AAATG	AGGATAACTATGGGAACCTTCAACTCCGACAGATATGATTTGGCGGATTCATGAG	1875
QY	906	ATTAG	ATTTCTGTATGAGAGCACTGAATGTTATGGAGAGCAAAATCAGATCTCTAATAA	965
Db	1876	ACTTG	ACTCTGCACTATGAGGGCGTTGAATGTGTGAGAGCAAAACCTGATCTCTAATA	1935
QY	966	AAATTT	TAGCTTTGCTGTGAATAGACGCTACTGCTGGAATGGGTAAAGGTT	1025
Db	1936	GAAAT	TCAGTTTGGTCTCATGAACAGACATGACCGCAGGGATGGTAAAGACT	1995
QY	1026	ATTGC	ACATGTGGCTCAAGCAACCTTTACTAGATGTAGAAGAGATTAACGTGAGGCTGGA	1085
Db	1996	GCTTC	ATATGTGGCTGAGCAACCCCTCGTGAATTTGAATGAGATTAAGACGAGATTAGA	2055
QY	1086	TTTTG	TCAATCATCTGTGGAGGATCTCGCTTGCCCAAGATTTGAGCGAGCAATCTGAA	1145
Db	2056	TATAG	TTCAGTGTTTGGTTGAAGAGCTGGGTTAAGGCCAGGATCTTAGACAGCATCTGAA	2115
QY	1146	AAGAAT	TTCAGATATTGAGGGCTGACACAACTCTTGAGAGGAAGAGCCAGTTTACT	1205
Db	2116	GCGAAT	CTCAGATGTTTGAAGGCTTTTGGCGAGTCTCGAGAGAAGAGAGGTGGGTACA	2175
QY	1206	GCACTG	TGAAAACTCTAT-----	1224
Db	2176	GCAAT	TATTAACCTCTATCAGGTACTTTCCGCACTTCAATCTGCTCTCTCAATGTTAA	2235
QY	1225	-----	-----	1224

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Db 2236 CAAAATTGCATTTTCATTTGTCCTAAATGCTGTTTATGCAACTCTGAACTTATAGGTATGTT 2295
Qy 1225 -----CAGTCAAGTACGAGTACCA 1245
Db 2296 ATTAAGTTCAATTAAGTCTTCTCTCTGAGTCAGCTATAAGGCTTCCC 2355
Qy 1246 TATATCAAAAGTGTGTTGGACGTCNTGATGGCAATTCGCAACTCATCAGGGAAGG 1305
Db 2356 TTCAATCAAAACAGCTATGCAACAGTACACCGGAGAAATTCGATCACTCATCAGGAGAGG 2415
Qy 1306 TATATGATTTCTTAGAGAAATGGAGTGATGATTAATCACCTGGAATAAGTTTCATAGGTCTT 1365
Db 2416 TACCTGAAAAAGCTTGGAGCTTTATCAGATCAAGATCACCTTGGAAAGTTTCATCGATTG 2475
Qy 1366 GTGGAACACTTCTGTGACCTTGATCACTTGGAGATGGAGAAATCATGATTTCTTCTGCA 1425
Db 2476 GTTGAGTGCTCTGAGATCTTGGACGCTAGAAATGGAGAAATCATGATATCTTCAAC 2535
Qy 1426 TATGACCCAAATTTATCTGCTCTGAAGATGAGCAAGAGACATTTGGAGCGCAAAATTCAT 1485
Db 2536 TAGGACACCAATTTGGCATCTCTGAAAGATCAGAAAGATTTGCTGGAGAGCAATTCAC 2595
Qy 1486 AATTGACCAAACTGCAAACTGCAATGATCTTGTATCTACCTATTGATAAGTCACTTTAAACTA 1545
Db 2596 GAATTGCACAAAAGACAGCGATAGAACTTGATCTTCAGGTCGACAAAGGCTCTTAAACTT 2655
Qy 1546 GATTAAGAAACAAATTTGACACGCTCTTCAAAATACCAAGAAAGAAACCAAAAGTC 1605
Db 2656 GACAAAGCGCGCAATTTGGCATGCTTTCAGGATCAGAAAGATCGAAAGAGGAGCCAAAGATC 2715
Qy 1606 AGGAGAGAGCTAAATTTCTCACTACATTTGCTCGAAACAGTAAAGGATGGGTAAGTTC 1665
Db 2716 AGGAGAGAGCTGACGACACAGTTTATAGTCTGGAGACTCCAAAGAGGAGTGAGTTC 2775
Qy 1666 ACCTATACAAACTCAAAACTAGGAGATCAGTTTCCAGAGATTTGAGAGGAGTACAAA 1725
Db 2776 ACAAACAAAGCTAAAAACTGGCGACAGTACCAAGTGTGTGATGATTATAGG 2835
Qy 1726 AGCTGTGAGAAAGATTTGAGTACGTTGATGTTCAACAGCTGCGAGTTTCTCGAGGTG 1785
Db 2836 AGCTGTGAGAAAGAGCTGTTGATGTTGATGTTGAGACTGTTACAGCTTCTCTGAGGTA 2895
Qy 1786 TTTCAGGTAT 1796
Db 2896 TGTTTAGTTAT 2906

RESULT 8
US-10-424-599-141791
; Sequence 141791, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 141791
; LENGTH: 1124
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1124)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_99049C.1

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US-10-424-599-141791

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Query Match 20.7%; Score 627.6; DB 12; Length 1124;
Best Local Similarity 76.1%; Pred. No. 3.5e-165;
Matches 785; Conservative 0; Mismatches 246; Indels 1; Gaps 1;

Qy 37 GAGGAACAGAGCAGCTTCCGAGCTTAACTCGATGCTAAGCAAGCTCAAGGATTTCTC 96
Db 92 GACCTAAATAAATAACTCCCTGAGCTCAAAATTAAGTCTTAAGCAAGCGAAGGTTTCTG 151
Qy 97 TCATTTCTTCAAAACCCCTGCCCCAAGGACCCCTAGGCGCAGTTGCGCTCTTTGATCGTCGGGAC 156
Db 152 TCATTTTCAAAACCCCTACCTGATGATCCAAAGGCTGTACGGTTTTTTGATCGCCGGAC 211
Qy 157 TATATATACATCTCATGGAGATGATGCAACTTTTCATTGCGAGAGACATATTAACCAACA 216
Db 212 TATTATATTGCCCATGGTGAATGCTACATTCATTGCAAAAGCCTATTATACCACTACT 271
Qy 217 ACTGCGTTACGACAGTTGGGTAAATAGAGCTGATGCCCTTTCCAGTGTAGTGTGAGTAGA 276
Db 272 ACAGCTATGCGACACTGGGCACTGGATCAATGCTCTTTCCAGTGTAGTGTGAGTAGA 331
Qy 277 AACATGTTTGAACAATPAGCTCGTGACATTTCTTTGGAGAGAAATGGACCGTACTCTTGA 336
Db 332 AACATGTTTGAACAATGCTCGTGATCTCTTTGGAGAGAAACAGACCATACTCTTTGAG 391
Qy 337 CTATATGAGGCGAGTGGTCAAACTGGAGACTGGTAAAGTGGAAACCCAGGGAATCTT 396
Db 392 CTCTATGAAGGTAGTGGTCTTAAATGGAGACTGGTCAAAAGTGGAAACACCTGTTAAT 451
Qy 397 GGAAGTTTTCAGGATATCTGTTTGTCTTAAATAAGTCAAAATCTCCGGTGATTGCT 456
Db 452 GGCAAGTTTGAAGATGTTCTGTTTGTCTTAACAGTGAAGTGAAGTCTCCAGTTGTT 511
Qy 457 GCTCTTCTCAAACTTCGGTCAAGATGATGTAAGTTCGGCTTAGCTATGTTGATATT 516
Db 512 GCTTTGTCACTTAACATATCGGAAATGGTGCACCATTTGGGTTAGGATTTGTTGATCTA 571
Qy 517 ACTAAGAGAGTCTTGGTTTAAACAGAAATTTCTAGATGATAGCCACTTCACAAATTTGG 576
Db 572 ACTAAGAGAGTACTTGGGATGGCTGAATTCCTTGTGACAGTCACTTCACAAATTTGG 631
Qy 577 TCTGCTTTGTTGCTCTTGGTTGACAGAAATGCTTGTACCGGAGAGCTGGCAAAATCC 636
Db 632 TCAGCATTTGTTGCACTTGGCGCAACAGTGCATTCGCTATAGATCTCGGGAATCT 691
Qy 637 AGTGAATACAGGCTATGTTTGTATGCA-ATATCTAGATGCGCGGTGATGTTAACTGAAG 695
Db 692 ACTGACAAATAGGATGTTGTGTATGTAGTTGACTAAATGTGTGTGATGTTAACTGAG 751
Qy 696 AAAGAAACTGAAATTTAAAGGGAGAGATTTGGTACAGGATCTTGGTAGGCTCGTCAAGG 755
Db 752 AGAGAAATCTGAAATTTAGAACTAGGATCTGGTACAGGATCTTGGCAGGCTTGTAAAG 811
Qy 756 TTCAGTAGAACCTGTTTCGAGATTTGGTCTCTGGGTTTCGAAATGTGCATCAGCGCTTTGG 815
Db 812 CCCTATTGAACAGTTCGAGATTTAGTCTCTGATTTGGATCTGCACCTGGTCTTAGG 871
Qy 816 GTGCATATCTTCTTATGCAAACTACTTGGCGATGAGAGCAACTATGGAACCTATACAGT 875
Db 872 GGCATTACTATCTTATGCAAGTACTTGGCAGATGAAAGCAATTAAGAAATTAATACTCT 931
Qy 876 CAAACATACAACTCAATAGTTTACATGATGATTTAGTCTGCTGCTATGAGCACTGAA 935
Db 932 GCGTAGTTTCAATCTTGACAGCTACATGAGTTAGACTCTGACGCCATGAGACCTTAA 991
Qy 936 TGTATTGAGAGCAAAATCAGATGCTAATAAAAAATTTTAGCTTGTTCGGTCTGATGATAG 995
Db 992 TGTCTTGNAAAGCAAACTGATGCAAAACAAAATTTTCAGTTTGTGTTCTCATGATAG 1051
Qy 996 AACGTGTACTGCTGGAATGGTAAAAAGTTTATTCACATGCTGGAAGCAACCTTACT 1055
Db 1052 GACTTGTACTGCTGGAATGGAAAAAGGNTATTTGACGCTCTGCTGCTGCTGCTGCTGCT 1111

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QY 2024 ACATGGGTGGAAAGTCGACCTACATTCGGCAGGTGGTGTGAATGTCCTGATGCCCAAG 2083
 Db 2015 ATATGGGAGGTAAATCAACATATATTCGACAACTGGGGTGATAGTACTCATGSCCAAA 2074
 QY 2084 TTGGCTCGTTTGTTCATGTCGACATGCTACCATTTCTATTCGTGATGATTTTGTGTC 2143
 Db 2075 TTGGGTGTTTGTGTCATGTCGAGTCAGCAGCAAGTGTCCATTTGTGGACTGCACTTAGCCC 2134
 QY 2144 GTGTTGGCGCTGGAGATTGCCAGCTGACAGAGTTCCTACCTTTTATGCAAGAGATGCTTG 2203
 Db 2135 GAGTAGGGCTGGTGACATGCTAAATGGAAGAGTCTCCACGTTTATGGCTGAAATGTGG 2194
 QY 2204 AGACTGCATCGATCTTGAAAGAGACTACTGATAGATCATGATGATTAATGATGAGTTGG 2263
 Db 2195 AAACTGCTTCTATCCTCAGGTCGCAACCAAGATTCATTAATAATCATAGATGAATTGG 2254
 QY 2264 GCCGTGGGACATCAACCTPACCATGGCTTGGCTTTAGCTTGGGCTATTTGTGAGCACATTG 2323
 Db 2255 GAAAGGNACTTCTACCTPACCATGATTTGGGTGTAGCATGGGCTATATCGAATACATTG 2314
 QY 2324 TTGAAGAAATTAAGCAACCAATTTGTTGGCACTCACTTTTCATGAGCTGACTGCATTAG 2383
 Db 2315 CAACAAGATGTTGCTTTTTCATGTTTGGCAACCCATTTTCATGAATTTACTGCTTGG 2374
 QY 2384 CCAACAGATGGAGACATGACATAGAAAATGCTGGGATAGCAAAATTTTCATGTTT 2443
 Db 2375 CCAATCAG-----ATACCAACTGTTAATAATCTACATGTCA 2410
 QY 2444 TTGCACACATTTGACCTTCTAATCGAAGCTAACTATGCTTTTACAGGTTTCAACCCAGTG 2503
 Db 2411 CAGACTCA-----CCACTGAGAGACCTTAACTATGCTTTTACAGTGAAGAAAGTG 2464
 QY 2504 CTTGTGATCAGAGTTTGGTATTCATGTTGCTGAAATTTGCAAAATTTCCACCGAGTGTG 2563
 Db 2465 TCTGTGATCAAGTTTGGGATTCATGTTGAGAGCTTGCTAAATTCCTTAAGCATGTAA 2524
 QY 2564 TGGCTCTGGCTAGAGAAAAGGCTGAGTTGGAGGATTTCTCTTATGCCCATAATTC 2623
 Db 2525 TAGAGTGTGCTTAAACAGAAAGCCCTGGAACTTGAGGAGTTTCAGTATATTTGGAGATCGC 2584
 QY 2624 CAATGACATTAAGAGGCGACCTTCAAAACGGAAGAGAGATTTGA 2669
 Db 2585 AAGGATATGATATCATGGAACAGCAGCAAGAAAGTGTATCTGGA 2630

RESULT 10
 US-10-062-674-1794
 ; Sequence 1794, Application US/10062674
 ; Publication No. US20040005559A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.
 ; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
 ; FILE REFERENCE: PA-0026-1 CIP
 ; CURRENT APPLICATION NUMBER: US/10/062,674
 ; CURRENT FILING DATE: 2002-01-30
 ; PRIOR APPLICATION NUMBER: US 09/625,102
 ; PRIOR FILING DATE: 2000-07-24
 ; NUMBER OF SEQ ID NOS: 2217
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 1794
 ; LENGTH: 3161
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20040005559A1 251562.5
 US-10-062-674-1794

Query Match 13.9%; Score 422.4; DB 15; Length 3161;
 Best Local Similarity 51.4%; Pred. No. 3.4e-107;
 Matches 1195; Conservative 0; Mismatches 1071; Indels 50; Gaps 7;
 QY 359 ACTGAGACTGGTAAAGTGGAACCCAGGGAATCTTGGAAAGTTTGGAGATATTCGT 418

Db 425 ATTGGTATTTGGCATATAAGGCTTCTCTCGCAATCTCTCTCAGTTTGAAGACATTTCTCT 484
 QY 419 TTGCTAATAATGAATGCAAAAATTTCTCGGTGATTTGCTCTTGGCTCCAAATTTGGTGC 478
 Db 485 TTGGTAACAATGATATGTCAGCTTCCATTTGGTGTGTGGGTGTTAAATGTCGCGAGTTG 544
 QY 479 AGAATGATCTGAAGTTGGCTTAGGCTATGCTATGATATTTACTAAGAGAGTCTTGGTTAA 538
 Db 545 ATGGCCAGACAGAGTTGGAGTTGGGTATGTGGANTCCATACAGAGGAAACTAGGACTGT 604
 QY 539 CAGAAATTTCTAGATGATAGCCACTTCAAAAATTTGGAGTCTTGGTTTGGTCTCTTGGTT 598
 Db 605 GTGAATTTCCCTGATATGATCAGTTCTTCCAATCTTGAAGCTCTCTCTCATCCAGATTGAC 664
 QY 599 GCAGAGATCTTGTGACAGCGGAGACTGGCAATCCAGTGAATACAGGCTATGTTTGG 658
 Db 665 CAAAGGAATGTGTTTACCCTGGAG- --GAGAGACTGCTGGAGACATGGGGAACCTGAGAC 721
 QY 659 ATGCAATATCTAGATGGCGCTGATGTAATCTGAAAGAAAGAACTGAAATTTAAAGGGA 718
 Db 722 AGATAATTTCAAGAGGAGGAATTTCTGATCAGAAAGAAAGAAAGCTGACTTTTCCACA 781
 QY 719 GAGATTTGTAAGGATCTTTGGTAGGCTCTGCAAGGTTTCA-----GTGAAC 766
 Db 782 AAGACATTTTATCAGGACCTCAACCGGTTGTTGAAAGGCAAAAGGAGAGCAGATGAATA 841
 QY 767 CTGTTGAGATTTGGTCTCTCGGTTTGAATTTGATGATCAGGCTTTGGGGTGACATCTTT 826
 Db 842 GTGCTGATTTGCCAGAAATGGAATCAGGTTGAGTTTTCATCACTGCTCTGCGGTAATCA 901
 QY 827 CTTATGACAGAACTACTTGGCGATGAGAGCAACTATGAAACTATACAGTCAAAACAATACA 886
 Db 902 AGTTTGTAGAACTCTTATCAGATGATTCGAATTTGGACAGTTTGAATGATGACTTCTTG 961
 QY 887 ACCTCAATAGTTATCAGATGATGATTTCTGCTATGAGAGCACTGAATTTGTTATGAGA 946
 Db 962 ACTTCAGCCAGTATATGAAATTTGATTTGAGCAGTCAAGCCCTTAACTTTTTCAGG 1021
 QY 947 GCAAACTCAGATGCTATATAAAATTTTGTGCTGATGATGATGATGATGATGATGATG 1006
 Db 1022 GTTCTGTTGAAGATACCACTGACTCTCAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 1081
 QY 1007 CTGGAATGGGTAAAGGTTTATTCACATGTTGGCTGAAAGCAACCTTTTACTAGATGAGAAG 1066
 Db 1082 CCCTCAAGGCAAAAGACTTTGTTAAACAGTGGATTAGCAGCTCTCTCATGATGAAGACA 1141
 QY 1067 AGATTAATCTGAGCTGGATTTAGTTCAATCAATGTTGGAGGATGCTGCTGCTGCTGCTG 1126
 Db 1142 GAATAGAGGAGAGATTGAAATTTAGTGAAGCTTTTGTAGAAGATGCAAAATTTGAGGAGA 1201
 QY 1127 ATTGAGGCAAGCAT--CTGAAAGAAATTTTCAATTTGAGCGGCTGACACACATCTTG 1183
 Db 1202 CTTTCAAGAGATTTTACTTCTGCTGATTTCCAGATCTTAAACCGCTTGGCAAGATTTTC 1261
 QY 1184 AGAGGAAAGAGCCAGTTTGTAGTCAAGTTGTAATAAATCTTATCAGTCAAGTACCAAGATAC 1243
 Db 1262 AAAGACAGCAGCAAACTTACAGATTTGTTACCGACTCTATCAGGGTATATAACTACTAC 1321
 QY 1244 CATATATCAAAAGTGTTTTGGAAAGCTCATGATGGGCAATTTGCAACACTCATCAGGAAA 1303
 Db 1322 CTAATGTTATACAGGCTCTGGAAAAACATGAAGAAAAACACAGAAATTTATTTGGCAG 1381
 QY 1304 GGTATATTGATTTCTTAGAGATGAGGTGATGATATCACCCTGATTAAGTTTCAATAGTTC 1363
 Db 1382 TTTTGTGACTCTCTTACTGTA-----TCTTGTGCTGACTTCTTCCAAAGTTTCAGAAA 1435
 QY 1364 TTCTGAAACTTCTGTTGACCTTTGATCAACTTGAAGATGAGAAATACATGATTTCTTCTG 1423
 Db 1436 TGATAGAAACAACTTTAGATATGATCAGGTGGAACCAATGATTTCTTGTAAACCTT 1495
 QY 1424 CATATGACCCAAATTTTATCTGCTCTCAAGGATGAGCAAGACATTTGGAGCGCAAAATTC 1483

Db 1496 CATTGTGATCCCTAATCTCAGTGAATTAAGAGAAATAATGAATGACTTGGAAAGAGATGC 1555
 QY 1484 ATAATTTGCAACAACAGCTGCGAATGATCTTGATCTTACCTATTGATTAAGTCACTTAAAC 1543
 Db 1556 AGTCAACATTAAATAGTGCAGCCAGAGATCTTGCTTGGACCCCTGGCAACAGATTAAAC 1615
 QY 1544 TAGATAAAGAAACACAATTTGGACAGCTCTTCCAGAAATTACCAAGAAAGAAACCAAAAG 1603
 Db 1616 TGGATTCAGGTGACAGTTGGATATTACTTTCGTGTAACCTGTAGGAAGAAAGTCC 1675
 QY 1604 TCAGAGAGAGCTAAATTTCTCACTACATTTGTTTCGAAACAAGTAAGATGGGGTAAAGT 1663
 Db 1676 TTCGTAA-----CAATAAATACTTTAGTACTGTAGATATCCAGAGAAATGGTGTAAAT 1729
 QY 1664 TCACCTATACAAACTCAAAAACCTAGGAGTCACTTCCAGAAATTTGTAGAGAGTACA 1723
 Db 1730 TTACCAACAGCAATTTGACTTTCTTTAAATGAAGAGTATACCAAAAATAAACAAGAAATG 1789
 QY 1724 AAAGCTGTCAAAAAGAAATTTGGTAGCTCGTGTAGTTTCAACAGCTGCGAGTTTCTCCGAGG 1783
 Db 1790 AAGAAGCCAGAGTCCATTTGTTAAGAAATTTGCAATATTTCTTCAGGCTATGTAGAC 1849
 QY 1784 TGTTCAGGTATAGCTGGTGTACTTGTGTAGTTGGATGTTTACTAGTTTTCGGGATT 1843
 Db 1850 CAATGACAGACTCAATGATGTGTAGCTCAGCTAGATGCTGTGTGCTGCTCAG 1909
 QY 1844 TGGCTGCCAGTTGCCAACCCTTACACAGACCAATATACAGTCCACCAAGATACAGAG 1903
 Db 1910 TGTCAATGAGACCTGTTCCATATGTACACAGCAGCCATTTTGGAGAAAGGACAGGAA 1969
 QY 1904 ATATTATCTTGAAGGCTAGGAGTCTGTTGTGGAAGCTCAAGATTTGGGTTAACTCCA 1963
 Db 1970 GAATTAATTAAAGAGCTCCAGGATGCTTGTGTGGAATTTCAAGATCAATTTGCAATTA 2029
 QY 1964 TTCTTAATGACTGTAGTACTAGTTAGGAGAGAGATTTGGTTTCAATATACAGAGCCCTA 2023
 Db 2030 TTCTTAATGACTGTATCTTTGAAAGAAATAAACAGATGTTCCACATCAATTAAGTCCCA 2089
 QY 2024 ACATGGTGGAAAGTCCAGCTTACATTCGGCAGGTTGGTGTGAATGCTGATGCCCCAAG 2083
 Db 2090 ATATGGGAGGTAAATCAACATATATTCGACAACTGGGGGTAGTAGTACTCATGCCCCAA 2149
 QY 2084 TTGCTGCTGTTTGTTCATGTGACAAATGCTACCAATTTCTATTGTTGATGTTATTTTGTCT 2143
 Db 2150 TTGGGTGTTTGTGCTGCAATGAGTGCAGAGAGTTCATTTGTGACTGCTATAGCCC 2209
 QY 2144 GTGTTGGCGCTGGAGATTCGACGTGAGAGAGTTTCTACTTTATGCAAGAGATGTTG 2203
 Db 2210 GAGTAGGGGCTGTGTGACAGTCAATTTGAAAGAGTCTCCACGTTTCATGGCTGAAATGTTG 2269
 QY 2204 AGACTGCATCGATCTTGAAGGAGCTACTGATAGATCATTTGATTAATTTGATGAGTTGG 2263
 Db 2270 AACTGCTTCTATCTCAGGTCTGCAACCAAGATTCATTAAATATCATGATGAATGG 2329
 QY 2264 GCGTGGGACATCAACCTACGATGGCTTGGTTTGTAGCTTGGGCTATTTGTGAGCACAATTG 2323
 Db 2330 GAAGAGGAATCTTCTACCTACGATGATTTGGTTAGCATGGGCTATATCAGATACATTG 2389
 QY 2324 TTGAAGAAATTAAGACCAACATTTGTTGCACTCTCTTTCATGAGCTGACTGCATTAG 2383
 Db 2390 CAACAAAGATTTGGTCTTTTTCATGATGTTTGAACCCATTTTCATGAACTTACTGCCTTG 2449
 QY 2384 CCAACAGATGGAGACAAATGCAATAAGAAATGCTGGGATGCAAAATTTTCATGCTTT 2443
 Db 2450 CCAATCAG-----ATACCAACTGTTAAATATCATATGCA 2485
 QY 2444 TTGCACACATTTGACCCCTTCTAATCGCAAGCTTAACTATGCTTTTACAAGTTTCAACCGGTG 2503
 Db 2486 CAGCACTCA-----CCACTGAAGAGACCTTAACTATGCTTTTATCAGGTGAGAAAGGTG 2539
 QY 2504 CTTGTGATCAGAGTTTGGTATTCATGTTGCTGAATTTGCAAAATTTTCCACCGAGTGTG 2563
 Db 2540 TCTGTGATCAAAAGTTTGGGATTCATGTTGAGAGCTTGCTTAATTTCCCTAAGCATGTAA 2599

QY 2564 TGGCTCTGGCTAGAGAAAGGCATCTCAGTTGGAGGATTTCTCTCCATTATTGCCAATATTC 2623
 Db 2600 TAGAGTGTGCTAAACAGAAAGCCCTCGAACTTGGAGGATTTCTAGTATATTGGAGATCGC 2659
 QY 2624 CAAATGACATTAAGAGCGCAGCTTCAAAACGGAAGAGAGATTTGA 2669
 Db 2660 AAGGATGATATCATGGAACCCAGCAGCAAAAGAGTCTATCTGGA 2705

RESULT 11

US-10-109-791A-3
 ; Sequence 3, Application US/10109791A
 ; Publication No. US20030138787A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Biotech OncoLogic Corp.
 ; TITLE OF INVENTION: Functional Genetic Tests of DNA Mismatch Repair
 ; FILE REFERENCE: BTOL 102 NP
 ; CURRENT APPLICATION NUMBER: US/10/109,791A
 ; CURRENT FILING DATE: 2002-09-06
 ; NUMBER OF SEQ ID NOS: 315
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 2805
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-109-791A-3

Query Match 13.9%; Score 420.8; DB 14; Length 2805;
 Best Local Similarity 51.3%; Pred. No. 8.8e-107;
 Matches 1194; Conservative 0; Mismatches 1072; Indels 60; Gaps 7;

QY 359 ACTGAGACTGTGTAAGTGGAAACCCAGGGAACTTTGGAAGTTTGGAGATATTCGT 418
 Db 347 ATTGGTATTTGGCATATAAGGCTTCTCTCGCAATCTCTCAGTTTGAAGACATTTCT 406
 QY 419 TTGCTAATTAAGAAATGCAAAATTTCCGGTGATTTGCTCTTGTCTCCAACTTCGGTC 478
 Db 407 TTGGTAACAATGATATGTCAGTTTCCATTTGGTGTGGGTGTTAAATCTCCGACATTG 466
 QY 479 AGAATGGATGTGAAGTTGGCTTAGGCTATCTTGATATTAATAAGAGAGTCTTTGGTTAA 538
 Db 467 ATGCCAGACAGACAGTTGGATTTGGGTATGTGATTCATACAGAGAAACTAGACTGT 526
 QY 539 CAGATTTCTAGATGATAGCCACTTCAAAATTTGGAGTCTGCTTTGGTCTCTTGGTT 598
 Db 527 GTGAATTTCCCTGATATATGATCAGTTTCTCAATCTTGAGGCTCTCTCATCAGATTGGAC 586
 QY 599 GCAGAGAAATGCTTTGTACACGCGGAGACTGGCAAAATCCAGTGAATACAGGCTATGTTG 658
 Db 587 CAAGGAATGTGTTTACCCGGAG---GAGAGACTGCTGGAGACATGGGAAACTGAGAC 643
 QY 659 ATGCAATATCTAGATGCGGCTGATGATGTAATCTGAAAGAAAGAAACTGAATTTAAAGGA 718
 Db 644 AGATAATTTCAAGAGGAGGAATTTCTGATCAGAGAAAGAAAGAAAGCTGATTTTCCCAA 703
 QY 719 GAGATTTGGTACAGGATCTTTGAGGCTCGTCAAGGGTCTCA-----GTAGAAC 766
 Db 704 AAGACATTTATCAGGACCTCAACCGGTTGTTGAAGGCAAAAGGAGGAGACAGATGAATA 763
 QY 767 CTGTTGAGATTTGGTCTCTTGGGTTCGAATGTCATCAGGCGCTTTGGGGTGCATATCTTT 826
 Db 764 GTCTGTATTGCCAGAAATGGAGAAATCAGTTGCGAGTTTTCATCTGCTGCGGTAATCA 823
 QY 827 CTTATGCAAACTACTTGGGGATGAGAGCAACTATGGAACACTATACAGTCAAAACATACA 886
 Db 824 AGTTTTTGAAGACTCTTATCAGATGATTTCCAATTTGGACAGTTTGAATGACTACTTTTG 883
 QY 887 ACCTCAATGTTACATGAGATTTAGATTTCTGCTGATGAGAGACATGAATTTGTTATGAGA 946
 Db 884 ACTTCAGCAGTATATGAATTTGSAATTTGAGATTTGAGCAGCTCAGAGCCCTTAACTTTTTCAGG 943
 QY 947 GCAATCAGATGCTTAATAAATTTTAGCTTGTTCGTTGATGAATAGAACCGTGTACTG 1006

Db 944 GTTCGTGTAAGATACCACTGGCTCTCAGTCTCTGGCTCGCTGCTGAATAAGTGAATA 1003
 Qy 1007 CTGGAATGGGTAAAGGTATATGACATGTGGCTGAGCAACCTTTACTAGATAGAG 1066
 Db 1004 CCCCTCAAGGCAAGACTCTGTTAAACCGATGGATTAAGCAGCCTCTCATGATGAAGA 1063
 Qy 1067 AGATTAACTGTAGGCTGGATTAGTTCAATCAATCGTGGAGGATGCTCGCTTCGCCAAG 1126
 Db 1064 GAATAGAGGAGAGATTGAATTTAGTGGAGCTTTGTAGAGATGCGAATTTGAGGCGA 1123
 Qy 1127 ATTTGAGGACAT---CTGAAAAGAAATTCAGATATTGAGCGGCTGACACAAATCTTG 1183
 Db 1124 CTTTACAAAGAAATTTACTTCGTGATTCCTCCAGATCTTAACCGACTTCCCAAGATTTT 1183
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 Db 1184 AAAGACAGCAGCAACTTCAAGATTGTTACCGACTTATCAGGGTATAAATCAACTAC 1243
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 Qy 1304 GGTATATGATCTCTAGAGAAATGGAGTGAATGATATCACTGAAATGATTCATAGTC 1363
 Db 1304 TTTTGTGACTCTCTTACTGA-----TCTTCGTCTGACTTCTCCAAAGTTTCAGGAAA 1357
 Qy 1364 TTGTGGAACCTCTGTGACCTTGATCACTGAGATGGAGATACATGTTTCTCTG 1423
 Db 1358 TGNATGAAACATTTAGATGATGATGAGTGGGAAACCATGAAATTCCTGTAACACCTT 1417
 Qy 1424 CATATGACCCAAATTTATCTCTCTGAGGATGAGCAAGACATTTGAGCGACAAATTC 1483
 Db 1418 CATTTGATCTTAATCTCAGTGAATTAAGAGAAATAATGAAATGCTTGGAAAGAGATGC 1477
 Qy 1484 ATAAATTTGCAAAACAACTGCCAATGATCTGATCTTACCTATTGATTAAGTCACTTAAAC 1543
 Db 1478 AGTCAACATTAATAGTGCAGCCAGAGATCTTGGCTTGGACCTTGGCAAAACAGATTAAC 1537
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 Qy 1604 TCAGGAAGCAGCTAAATTTCTCACTACATTTGTTCTGAAACACGTAAGATGGGTAAAGT 1663
 Db 1598 TCTGTAA-----CAATAAAACCTTAGTACTGTAGATATCCAGAGAAATGTTTAAAT 1651
 Qy 1664 TCACCTATACAAACTCAAAACCTAGAGATCAGTCCAGAAATTTGTAGAGAGTACA 1723
 Db 1652 TTACCAACAGCAATTTGACTCTTTTAAATGAAGATATACCAAAATTAACACAGAAATG 1711
 Qy 1724 AAAGCTGTCAAGAAAGAAATTTGATCTGCTGTAGTTTCAACAGCTGCGAGTTTCTCCGAG 1783
 Db 1712 AAGAGCCAGATGCCATTTGTAAGAAATTTGCAATTTCTTCAGGCTATGAGAAC 1771
 Qy 1784 TGTGTCAGGTATAGTGGTGTACTGCTGAGTTGGATGTTGTTACTGAGTTTTCGGATT 1843
 Db 1772 CAATGCAACACTCAATGATGTTGCTGCTAGTATGCTGTTGTCAGCTTGTCTCAG 1831
 Qy 1844 TGGCTGCAGTTGCCAACTCCCTACACAGAACCAATATCAGTCCACCATATACAGAG 1903
 Db 1832 TGTCAATGGAGCACTCTTCCATATGATACGACCCAGCCATTTTGGAGAAAGCAAGAA 1891
 Qy 1904 ATATTATCTTGAAGGTTGAGGATCTCTGTTGAGAGCTCAAGATTGGGTAACTCCA 1963
 Db 1892 GAATATATTAAGCATCCAGGCATGCTGTTGTAAGATTCAAGATGAATTTGCAATTA 1951
 Qy 1964 TTCTTAATGACTGTAGTACTGTTAGGGGAGAGAGTTGGTTTTCAGATTATCACAGCCCTA 2023
 Db 1952 TTCTTAATGACTGTATCTTGAAGAAAGATAACAGATGTTCCACATCTTACTGCCCCA 2011
 Qy 2024 ACATGGGTGAAAGTGCACCTTACATTCGGCAGGTTGGTGTGAATGCTCTGATGCCCAAG 2083

Db 2012 ATATGGAGGTAATCAACATATATTCGACAAACCTGGGGTGATAGTACTCATGTCGCCAAA 2071
 Qy 2084 TTGGCTGTTGTTCCATGTGACAAATGCTACCAATTTCTATTTCGTGATTGTTTCTC 2143
 Db 2072 TTGGGTGTTTGTGCTCAATGTAGTACAGAAAGTGTCCATTTGTGAGTGTGATCTTAGCCC 2131
 Qy 2144 GTGTGTCGCTGGAGATTGCCAGCTGAGAGAGTTTCTTACTTTTATGCAAGAGATGCTTG 2203
 Db 2132 GAGTAGGGCTGGTGACAGTCAATTTGAAGAGAGTCTCCAGTTCATGCTGAAATGTTG 2191
 Qy 2204 AGACTGATCAATCTTGAAGAGAGTACTGATAGATCAATGATTAATTAATGATGAGTTGG 2263
 Db 2192 AAATGCTCTTCTCAGGTCTGCAACCAAGATTTCAATTAATCATAGATGAATGG 2251
 Qy 2264 GCGTGGGACATCAACCTCAGATGGCTTGGTTTGTAGCTTGGGCTATTTGTGAGCACATTG 2323
 Db 2252 GAGAGGAATCTTACCTCAGATGATTTGGTTGTAGCATGAGTGTGAGTGTATATCAGAAATACATTG 2311
 Qy 2324 TTGAAGAAATTTAAAGCAACCAATTTGTCCTCACTCACTTTCATGAGCTGACTGCATTAG 2383
 Db 2312 CAACAAAGATTTGGTGTCTTTTTCATGTTTTCGCACTGTTTCAACCCATTTTCACTGCTTGG 2371
 Qy 2384 CCAACAAAGATTTGAGACAAATGAGACATGAAGAAATGCTGGGATAGCAAAATTTTCTGTTT 2443
 Db 2372 CCAATCAG-----ATACCAACTGTTTAATAATCTCATGTCA 2407
 Qy 2444 TTGCACACATTTGACCTTTCTAATCGCAAGCTTAATGCTTTTCAAGGTTTCAACCCAGGTG 2503
 Db 2408 CAGCACTCA-----CCATGAGAGACCTTAATGCTTATGCTTTATCAGGTGAGAAAGGTG 2451
 Qy 2504 CTTGTGATCAGAGTTTGTGATTTCAATGTTGCTGAATTTGCAAAATTTTCCACCGAGTGTG 2563
 Db 2462 TCTGTGATCAAGTTTGTGGGATTCATGTCGAGAGCTTGTCTTAATTTCCCTAAGCATGTAA 2521
 Qy 2564 TGGCTCTGGCTAGAGAAAGCATCTGAGTTGGAGGATTTCTCTCTATTGTCCTAATTTTC 2623
 Db 2522 TAGAGTGTCTAAACAGAAAGCCCTGGAACCTGAGGAGTTTTCAGTATATTGGAGATCGC 2581
 Qy 2624 CAATGACATTAAGAGGCGAGCTTCAAAACGGAAGAGAGATTTGA 2669
 Db 2582 AAGATATGATATCATGGAACCCAGCAGCAAGAGTGTCTATCTGGA 2627

RESULT 12

US-09-788-657-9, Application US/09788657
 ; Sequence 9, Patent No. US20020123149A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nicolaides, Nicholas
 ; APPLICANT: Sasse, Philip
 ; APPLICANT: Kinzler, Kenneth
 ; APPLICANT: Grasso, Luigi
 ; APPLICANT: Vogelstein, Bert
 ; TITLE OF INVENTION: Methods for generating hypermutable
 ; FILE OF INVENTION: Yeast
 ; FILE REFERENCE: 01107.00097
 ; CURRENT APPLICATION NUMBER: US/09/788,657
 ; CURRENT FILING DATE: 2001-02-21
 ; PRIOR APPLICATION NUMBER: 60/184,336
 ; PRIOR FILING DATE: 2000-02-23
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: Fast-Seq for Windows Version 3.0
 ; SEQ ID NO 9
 ; LENGTH: 3145
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-788-657-9

Query Match 13.9%; Score 420.8; DB 9; Length 3145;
 Best Local Similarity 51.3%; Pred. No. 9 6e-107;
 Matches 1194; Conservative 0; Mismatches 1072; Indels 60; Gaps 7;

Qy 359 ACTGGAGACTGGTAAAGGTGGAACCCAGGGAATCTTGGAGTTTGTGAGGATATTCTGT 418

Db	415	ATTGGTATTGGCATATAAGGCTTCTCTCGCAATCTCTCAGTTTGAAGACAATTCTCT	474
Qy	419	TTGCTAATAATGAATGCAGAAATCTCCGGTGATTGCTGCTCTGCTCCAAACTTCGGTC	478
Db	475	TTGTTAAACATGATATGTCAGCTTCCATTGGTGTGTGGGTGTTAAATGTCGCGAGTTG	534
Qy	479	AGAAATGGATGTGAAGTTGGCTTAGGCTATGTTGATATTAATAAGAGAGTCTTTGGTTAA	538
Db	535	ATGCCACAGACAGGTTGGAGTTGGGTATGTGGATTCATACAGAGGAACTAGGACTGT	594
Qy	539	CAGAAATTTCTAGATGATAGCCACTTCACAAATTTGGAGTCTGCTTTGGTTCCTTGGTT	598
Db	595	GTGAATTTCCCTGATTAATGATCAGTTTCTCCAACTTTGAGGCTCTCTCATCCAGATTGGAC	654
Qy	599	GCAGAGAAATGCTTGTGTACACGCGGAGACTGCAAAATCCAGTGAATAACAGGCCATGTTTG	658
Db	655	CAAGGAATGTGTTTACCCGGAG--GAGAGACTGCTGGAGACATGGGGAACATGAGAC	711
Qy	659	ATGCAATPATCTAGATCGCGGTGATGTTAACTGAAGAAGAAACATGAATTTAAAGGGA	718
Db	712	AGATAATCAAGAGGAGGAATCTGATACAGAAAGAAATAAAGCTGACTTTTCCACAA	771
Qy	719	GAGATTTGGTACAGGATCTTGTGAGGCTGCTCAAGGTTCA-----GTAGAAC	766
Db	772	AAGACATTTATCAGGACCTCAACCGGTTGTTGAAGGCCAAAGAGGAGACGATGAATA	831
Qy	767	CTGTTCCAGATTTGGTCTCTGGGTTCGAATGTGCATCAGGCGCTTTGGGTGTCATCTTT	826
Db	832	GTGCTGTATTGCCAGAAATGGAGNATCAGGTTGCAGTTTCATCACTCTCGCGGTATCA	891
Qy	827	CTTATGCAGAACTACTTGGCGATGAGAGCAACTATGGAACATATACAGTCAAAACATACA	886
Db	892	AGTTTTTAGAACTCTTATCAGATGATTCCTCAACTTTTGGACAGTTTGAACCTGACTTTTG	951
Qy	887	ACCTCAATAGTTTACATGAGATTAGATTCTGCTGCTATGAGAGACCTGAATGTTATGGAGA	946
Db	952	ACTTCACCCAGTATATGAATTTGGATATTGCAGCAGTCAGAGCCCTTAACTTTTTCAGG	1011
Qy	947	GCAAACTCAGATGCTTAATAAAATTTTAGCTTGTTCGGTCTGTGATGAATAGAACCTGTACTG	1006
Db	1012	GTTCCTGTGTGAAGATACCACTGCGCTCTCAGTCTCTGGCTGCTTGTGATTAAGTTGAAA	1071
Qy	1007	CTGGAATGGGTAAAAGGTTATTGCACATGTGGCTGAAGCAACCTTTACTAGATGTAGAAG	1066
Db	1072	CCCTCAAGGACAAAGACTTGTTAAACAGTGGATTAAAGCAGCCTCTCATGTGATAAGAAC	1131
Qy	1067	AGATTAACTTAGGCTGATTTAGTTCAATCATCTGTGGAGGATGTCGCGCTTCGCCAAG	1126
Db	1132	GAATAGAGGAGAGATTGAATTTTAGTGGAACTTTTGTAGAGATGTCAGAAATTCAGGCAGA	1191
Qy	1127	ATTTTGGGCGAGCAT---CTGAAAAGAAATTCAGATATTGACGGCTGCACACAACTCTTG	1183
Db	1192	CTTTTCAAGAGATTACTTCTGTCGATTCACAGATCTTAACCGACTTCGCAAGATTTTC	1251
Qy	1184	AGAGGAAAAGAGCCAGTTTATGTCAGCTTGTAATAACTCTATCAGTCAAGTACCAGAGTAC	1243
Db	1252	AAAGACAAGCAGCAAACTTACAAGATTGTTTACCGACTCTATCAGGGTATAAATCAACTAC	1311
Qy	1244	CATATATCAAAAGTGTTTTGGAAAGCTCATGATGGGCAATTTGCAACTCATCAGGGAAA	1303
Db	1312	CTAATGTATTACAGGCTCTGGAAAAACATGAAGGAAAAACCCAGAAATTTATGTTGGCAG	1371
Qy	1304	GGTATATTGATCTCTAGAGAAATGGAGTGATGATTAATCACTTGAAATAGTTCATAGGTC	1363
Db	1372	TTTTTGTGACTCCTTACTGA-----TCTGCTCTGACTTCTCCAGTTTCAGGAAA	1425
Qy	1364	TTGTGGAACCTCTGTTGACCTTGATCAACTTGAGAAATGAGAAATCATGATTTCTTCG	1423
Db	1426	TGATAGAAAACACTTTAGATATGATCAGGTGGAAACCATGATTTCTTGTAAAAACCTT	1485
Qy	1424	CATATGACCCAAATTTTATCTGCTGTGAAGGATGAGCAAGAGACATTTGGAGCGCAAAATTC	1483

Db	1486	CA	TTTGATCTCTAATCTCAGTGAATTAAGAGAAATAATGAATGACTTTGGAAAAAGAGATGC	1543
Qy	1484	ATA	TTTGGCAAAACAAACCTGCCAATGATCTTGATCTTACCTATTGTATAAGTCACTCTAAAC	1543
Db	1546	AGT	CAACATTAATAAGTGCAGCCAGAGATCTTGCTTGGACCTTGGCAACAGATTAAAC	1505
Qy	1544	TAG	ATAAAGAAACACAAATTTTGGACACGTCTTCAGAAATTACCAAGAAGAAACCCAAAAG	1603
Db	1606	TGG	ATTCAGTGCCAGCTTTTGGATAATTACTTTCTGTGTAACTCTGTAAAGAAAGAAAAGTCC	1665
Qy	1604	TCAG	GAAGCAGCTAAATTTCTCACTACATTTGTTCTCGAACAAGTAAGGATGGGGTAAAGT	1663
Db	1666	TT	CGTAA-----CAATATAAAACTTTTAGTACTCTGTAGATATCCAGAAGAAATGSGTGTAAAT	1719
Qy	1664	TCAC	TATACAAAATCTCAAAAACCTAGGACATCAGTTTCCAGAAAGATTGTAGAGAGATACA	1723
Db	1720	TTAC	CAACAGCAATATGAGCTTTCTTTAATAGAGAGTATACCAAAATATAAACAAGATATG	1779
Qy	1724	AAAG	CTGTCTGAGAAGAAATGGTAGTCTGTTAGTTCAAACAGCTGCGAGTTTCTCCBAGG	1783
Db	1780	AAGA	AGCCAGGATGCCATTTGTTAAAGAAATTTGTCAATATTTCTTCAGGCTATGTAGAAC	1839
Qy	1784	TGTT	GCAGGTATAGCTGGTGTACTTGCTCAGTTTGGATGTGTACTAGATTTTCCGGATT	1843
Db	1840	CAAT	GCAGACACTCAATGATGTGTAGCTCAGCTAGATGCTGTGTGACGTTTTGCTCAAG	1899
Qy	1844	TGG	CTGCCAGTTGCCAACTCCCTTACACAAAGACCAAAATATCAGTCCACACAGATACAGGAG	1903
Db	1900	TGT	CAATAGAGCNCCTGTTTCCATATGTACGACCGCCATTTTGGAGAAAGGACAGGAA	1959
Qy	1904	ATA	TATATCTTGAAGGGTGTAGGCATCCTTTGTGTGAAGCTCAAGATTTGGTTAACTCCA	1963
Db	1960	GAA	TATATAAAGCATCCAGGCATCTTGTGTGAAGTTTCAAGATGAAATGTCATTTA	2019
Qy	1964	TT	CTAATGACTGTAGACTAGTTAGGGAGAGAGTTGGTTTTCAGATTAACAAGGCCCTTA	2023
Db	2020	TT	CTAATGACGTATACTTTTGA AAAAGATAAACAGATTTTCCACATCAITACTTGGCCCCA	2079
Qy	2024	ACAT	GGGTGAAAGTGCACCTACATTCGGCAGGTTGGTGTGAATGTCCTGATCGGCCCAAG	2083
Db	2080	ATAT	GGGAGTAAATCAACATATAATTCGACAAACTGGGGTGAATAGTACTCATGGCCCCAA	2139
Qy	2084	TT	GCTCGTTTGTTCATGTGACAATGCTACCAATTTCTATTCTGTGATGTGTATTTTGCTC	2143
Db	2140	TT	GGTGTCTTTTGTGCCATGTGAGTCAGCAGAGTGTCCTATTGTGGACTGCATCTAGCCC	2199
Qy	2144	GT	TGTGGCGCTGGAGATTCGACCTGAGAGGATTTCTACTTTTATGCAAGAGATGCTTG	2203
Db	2200	GAG	TAGGGGCTGGTGACAGTCAATTGAAAGGAGCTCTCCAGTTTCATGGCTGAAATGTTGG	2259
Qy	2204	AGAC	TGATCGATCTTTGAAAGGAGCTACTGATAGATCATTGATTATAATTTGATGAGTTGG	2263
Db	2260	AA	CTGTTCTATCTCAGGCTGTGCAACCAAGATTCATTATAATCATAGATGAATTGG	2319
Qy	2264	GCG	TGGGACATCAACCTACGATGGCTTTGGTTTAGCTTTGGGCTATTGTTGAGCAATTG	2323
Db	2320	GA	GAGGAACTTCTACTACATGGATTTGGTTAGCATGGGCTATATCAGAATACTATG	2379
Qy	2324	TT	GAAGAAATTAAGACCAACAATGTTTGGCTCCTCATCTTCAATGAGCTGACTGCANTAG	2383
Db	2380	CA	CAAAAGATTGGTGTCTTTTGCATGTTTGCACCCCACTTTTCATGAACCTTACTGCTTGG	2439
Qy	2384	CC	ACAGATGGAGACATGGACATAAGAAAAATGCTGGGATAGCAAAATTTTCATGTTT	2443
Db	2440	CC	ATCAG-----ATACCAACTGTTTAATAATCATCATGCTCA	2475
Qy	2444	TT	GCACATTTGCCCTTCTAATTCGAAGCTAACTATGCTTTTACAGGTTTCCACCGGTG	2503
Db	2476	CAG	CACTCA-----CCACTGAAGAGACCTTAACATGCTTTATCAGGTGAAGAAAGTG	2529
Qy	2504	CT	TGTGATCAGATTTTGGTATTTCATGTTCTGCTGAATTTGCAAAATTTTCCACCGAGTTTG	2563
Db	2530	TC	TGTGATCAAGATTTTGGATTCATGTTGCGAGCTTCTTAATTTTCCCTTAAGCATGTA	2589

QY 2564 TGGCTCTGGCTAGAGAAAGGCATCTCAGTTGGAGGATTTCTCTCTCTATTGCCATAATTC 2623
 Db 2590 TAGAGTGTCTAAACACAAAGCCCTGGAACCTTGGAGGATTTCTAGTATATTGGAGATCGC 2649
 QY 2624 CAAATGACATTAAGAGCGCAGCTTCAAAACGGAAGAGAGAAATTTGA 2669
 Db 2650 AAGGATATGATATCATGGAACCCAGCAGCAAGAAAGTGTCTATCTGGA 2695

RESULT 13
 US-09-912-697-9
 ; Sequence 9, Application US/09912697
 ; Publication NO. US2003068808A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nicolaides, Nicholas C
 ; APPLICANT: Sassi, Philip M
 ; APPLICANT: Grasso, Luigi M
 ; APPLICANT: Kline, J Bradford
 ; TITLE OF INVENTION: METHODS FOR GENERATING ANTIBIOTIC RESISTANT MICROBES AND NOVEL
 ; FILE REFERENCE: MOR-0040
 ; CURRENT APPLICATION NUMBER: US/09/912,697
 ; CURRENT FILING DATE: 2001-07-25
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 9
 ; LENGTH: 3145
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-912-697-9

Query Match 13.9%; Score 420.8; DB 10; Length 3145;
 Best Local Similarity 51.3%; Pred. No. 9.6e-107; Indels 60; Gaps 7;
 Matches 1194; Conservative 0; Mismatches 1072;

QY 359 ACTGGAGACTGGTAAAGAGTGGAAAGCCCGAGGAAATCTTGGAAAGTTTGGAGATATCTGT 418
 Db 415 ATTGGTATTGGCATATAAGGCTTCTCTGGCAATCTCTCAGTTTGGAGACATCTCT 474
 QY 419 TTGCTAATTAATGAATGCAAAATTTCTCGGTGATGCTGCTCTGCTGCTCCAACTTCGGTC 478
 Db 475 TTGGTAAACAATGATGTGACCTTCCATTTGGTGTGTGGGTGTTAAATGTTCGCCAGTTG 534
 QY 479 AGAATGATGATGAAGTTGGCTTAGCTATGTTGATATTACTTAAGAGAGTCTCTGTTTAA 538
 Db 535 ATGCCAGAGACAGGTTGGATGGTATGGAATTCATACAGAGAACTAGACTGT 594
 QY 539 CAGAAATTTCTAGATGATAGCCACTTCAAAATTTGGAGTCTGCTTTGGTTGCTCTTGGTT 598
 Db 595 GTGAATTTCCCTGATAATGATCAGTTCTCCAATCTTGAGGCTCTCCTCATCCAGATTGGAC 654
 QY 599 GCAGAGATGCTTTGTACCAGCGAGACTGSCAAATCCAGTGAATACAGGCTATGTTG 658
 Db 655 CAAAGGAATGTGTTTACCCTGGAG---GAGAGACTGCTGGAGACATCGGGAAACTGAGAC 711
 QY 659 ATGCAATATCTAGATGCGGCTGATGTTAACTGAAAGAAAGAAAGAACTGAATTTAAAGGA 718
 Db 712 AGATTAATCAAGAGGAGGAATTTCTGATCAAGAAAGAAAGAAAGAACTGACTTTTCCCAA 771
 QY 719 GAGATTTGGTACAGGATCTTGGTAGGCTCGTCAAGGGTTCA-----GTAGAAC 766
 Db 772 AAGACATTTATCAGGACCTCAACCGTTGTTGAAAGGCAAAAGGGAGAGCAGATGAATA 831
 QY 767 CTGTTGAGATTTGGTCTCTGGTTGGAATGTGATCAGGCGCTTTGGGTGCAATCTTT 826
 Db 832 GTGCTGTATTGCCAGAAATGGAGAACTAGGTTGAGATTTTCATCACTGTCTGCGGTAATCA 891
 QY 827 CTTATGACAGAACTACTTCCGATGAGAGCAACTATGGAATCTATACAGTCAAAACAATACA 886
 Db 892 AGTTTTHAGAACTCTTATCAGATGATTTCCAACTTTGGACAGTTTGAATGACTACTTTTG 951
 QY 887 ACCTCAATAGTTACATGATGATTAATGATTTCTGCTCTATGAGAGCACTGAATGTTATGGAGA 946

Db 952 ACTTCAGCCAGATATGAATTTGGATATTGCAGCAGTCAGAGCCCTTAACCTTTTTCAGG 1011
 QY 947 GCAATTCAGATGCTAATTAATAAATTTTAGCTTGTTCGGTCTGATGAATAGAACGTGACTG 1006
 Db 1012 GTTCTCTTGAAGATACCACTGGCTCTCAGTCTCTGGCTGCTTCTGCTGAATTAAGTGTAAAA 1071
 QY 1007 CTGGAATGGTAAAGGTTATTGCATATGTGGCTGAAGCAACCTTTACTAGATGTAGAAG 1066
 Db 1072 CCCTCAAGGACAAAGACTTGTAAACAGTGGATTAAAGCAGCCTCTCATGATAAGAAC 1131
 QY 1067 AGATTAACGTAGCTGGATTTAGTTCAATCATCTGTGGAGGATGTCGCCCTTCGCCAAG 1126
 Db 1132 GAATAGAGGAGAGATTGAATTTAGTGAAGCTTTTGTAGAAGATGAGAAATTCAGGACGA 1191
 QY 1127 ATTTGAGGCGAGCAT---CTGAAAAGAAATTCAGATATTGAGCGGCTGACACACAATCTTG 1183
 Db 1192 CTTTCAAGAAGAAATTTACTTCGTGATTTCCAGATCTTAACCGACTTCGCAAGAAGTTTC 1251
 QY 1184 AGAGGAAAAGAGCCAGTTTGTAGTCAGCTTGTAAACCTCTATCAGTCAAGTACCAGAGTAC 1243
 Db 1252 AAAGACAGCAGCABACTTACAGATTGTACCAGCTCTATCAGGGTATATAATCAACTAC 1311
 QY 1244 CATATATCAAAAGTGTTTTGGAAAGCTCATGATGGCAATTTGCAACACTCATCAGGAAA 1303
 Db 1312 CTAATGTATACAGGCTCTGGAAGAAACATGAAGGAAAACACACAGAAATTTATTGTTGGCAG 1371
 QY 1304 GGTATATTGATTTCTAGAGAAATGGAGTATGATTAATCCTGTAATAGTTTCATAGGTC 1363
 Db 1372 TTTTGTGACTCTCTTACTGA-----TCTGCTGCTGACTTCTCCAGTTTCAGGAAA 1425
 QY 1364 TTCTGAAACTTCTGTTGACTTGTCACTTGAATTCAGAAATGGAGAAATACATGATTTCTTCTG 1423
 Db 1426 TGAATGAACAACTTTAGATATGATCAGTGGAAACCAATGATTTCTTGTAAACCTT 1485
 QY 1424 CATATGCCCCAAATTTATCTGCTCTGAAAGATGAGCAAGAGACATTTGGAGCGCAAAATTC 1483
 Db 1486 CAATTGATCTTAATCTCAGTGAATTAAGAGAAATTAATGAATGACTTGGAAAGAAAGATGC 1545
 QY 1484 ATAATTTGCACAAACAACTGCCAATGATCTTGATCTACCTATTGATTAAGTCACTTAAC 1543
 Db 1546 AGTCAACATTAATAGTGCAGCCAGAGATCTTGGCTTGGACCCCTGGCAACAGATTAAC 1605
 QY 1544 TAGATAAGAGAAAACAACTTTGGACACGCTCTTCAGAAATTCACAAAGAAAGAAACCAAAAG 1603
 Db 1606 TGGATTTCCAGTGCACAGTTTGGATATTACTTTCTGTTAACTCTGTAAGAAAGAAAGTCC 1665
 QY 1604 TCAGGAAGCAGCTAAATTTCTCACTCATTTGTTCTCGAAACACGTAAGGATGGGTAAAGT 1663
 Db 1666 TTGCTAA-----CAATAAAACTTTTAGTACTGTAGATATCCAGAGAAATGSGTGTAAAT 1719
 QY 1664 TCACCTATACAAACTCAAAACTAGGAGATCAGTTCCAGAAATTTGTAGAGGAGTACA 1723
 Db 1720 TTACCAACAGCAATTTGACTTCTTTAAAGAGATATACCAAAATTAACAGAGATATG 1779
 QY 1724 AAAGCTGTCAAGAAAGAAATTTGGTAGCTGCTAGTCTCAACAGCTGCGAGTTTCTCCAGG 1783
 Db 1780 AAGAGCCAGATGCAATTTGTTAAAGAAATTTGCAATTTTCTTCAGGCTATGTAGAAC 1839
 QY 1784 TGTTTGCAGGTAAGCTGGTGTACTTCTGAGTTGGATGTTGTTACTGAGTTTTCGGGAT 1843
 Db 1840 CAATGACAGACACTCAATGATGTGTAGTCTCAGCTAGATGCTGTTGTCAGCTTTGCTCACG 1899
 QY 1844 TGGCTGCCAGTTGCCCACTCCCTTACAAAGACCAAAATTCAGTCCACCAGATACAGGAG 1903
 Db 1900 TGTCAATGGAGACCTGTTTCCATATGTACGACAGCCATTTTGGAGAAAGGACAGGAA 1959
 QY 1904 ATATTATCTTGAAGGCTGTAGGATCTCTTGTGTGAAGCTCAAGATTTGGTTTAACTCCA 1963
 Db 1960 GAATTTATTAAGGCAATCCAGGCAATGCTTGTGTTGAGTTCAAGATTTCAATTTGCAATTA 2019
 QY 1964 TTCTTAATGACTGTAGACTAGTTAGGGGAGAGAGTTGGTTTTCAGATTATCACAGGCCCTA 2023

Db 2020 TTCCTAATGACGTATACCTTTGAAAGAGATAAACAAGATGTTCCACATCACTACTGCGCCCA 2079
Qy 2024 ACATGGGTGGAAGTCGACCTACATTCGGCAGGTTGGTGTGAATCTCTGATGCGCCCAAG 2083
Db 2080 ATATGGGAGGTAAATCAACATATATTCGACAACTGGGGTGTAGTACTCATGGCCCAAA 2139
Qy 2084 TTGGCTCGTTTGTTCCTCATGTGCAAGTCAACATTTCTATTCTGTTGATTTGTTGCTC 2143
Db 2140 TTGGGTGTTTGTGTCATGTGAGTCAGCAGAGAAGTGTCCATTGTGAGCTGCATCTAGCCC 2199
Qy 2144 GTGTGTGGCGCTGGAGATTGCCAGCTGAGAGGATTTCTACTTTTATGCAAGAGATGCTTG 2203
Db 2200 GAGTAGGGCTGGTGTGACAGTCAATTTGAAGGAGTCTCCACGTTCCATGCTGAAATGTTGG 2259
Qy 2204 AGACTGCATCGACTTTGAAAGGAGCTACTGATAGATCAATGATTAATTAATGATGATG 2263
Db 2260 AAATGCTTCTATCTCTAGGCTGCAACCAAGATTCAATTAATCAATGATGAATTTGG 2319
Qy 2264 GCGTGGGACATCAACCTACGATGGCTTTGGTTTAGCTTTGGCTTATTTGTGAGCACATTG 2323
Db 2320 GAAGAGGAACCTTCTACCTACGATGGATTTGGTTAGCATGGCTATATCAAGATACATTG 2379
Qy 2324 TTGAAGAAATTAAGACCAACATTTGTTGCCACTCTACTTTTCATGAGCTGACTGATAG 2383
Db 2380 CAACAAGATTTGGTCTTTTGGCATGTTTGGCAACCCATTTTCATGAACCTTACTGCTTGG 2439
Qy 2384 CCAACAAGATGAGAGCAATGGAACATAAGAAAATGCTGGGATAGCAAAATTTTCATGTTT 2443
Db 2440 CCAATCAG-----ATACCACTGTTAAATTAATCTACATGTCA 2475
Qy 2444 TTGCACATGACCTTCTAATCGCAAGTAACTATCTTTTACAAGTTTCAACCCAGTG 2503
Db 2476 CAGCACTCA-----CCACTGAAGAGACCTTAACTATGCTTTTATCAGTGAAGAAAGTG 2529
Qy 2504 CTCTGTATCAGATTTGTTGTTTCTGTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2563
Db 2530 TCTGTATCAAGATTTTGGGATTCATGTTGAGAGCTTGTCTAATTTCCCTAAGCATGTA 2589
Qy 2564 TGGCTCTGGCTAGAGAAAGGACATCTGATTTGGAGGATTTCTCTCTATTTGCCATATTC 2623
Db 2590 TAGAGTGTCTAACAAGAGCCCTGAACTTGAGGAGTTTCAGTATTTGGAGATTCGC 2649
Qy 2624 CAATGACATTAAGGCGAGCTTCAAAACGGAAGAGAGAAATTTGA 2669
Db 2650 AAGGATATGATATCATGGAACCAAGCAGCAAGAAAGTCTATCTGGA 2695

RESULT 14
US-09-760-285-21
; Sequence 21, Application US/09760285
; Publication No. US2003009197A1
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas C
; APPLICANT: Grasso, Luigi M
; APPLICANT: Sassi, Philip M
; TITLE OF INVENTION: CHEMICAL INHIBITORS OF MISMATCH REPAIR
; FILE REFERENCE: MOR-0017
; CURRENT APPLICATION NUMBER: US/09/760,285
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 21
; LENGTH: 3145
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-760-285-21

Query Match 13.9%; Score 420.8; DB 10; Length 3145;
Best Local Similarity 51.3%; Pred. No. 9,6e-107;
Matches 1194; Conservative 0; Mismatches 1072; Indels 60; Gaps 7;
Qy 359 ACTGGAGACTGGTAAAGTGAACCCCAAGGAATCTTGGAAATTTTGGAGTATTTCTGT 418

Db 415 ATTGTATTTGGCATATAAGGCTTCTCCTGGCAATCTCTCTCAGTTTGAAGACATTTCTCT 474
Qy 419 TTGCTAATTAATGAATGCAAAATTTCTCGGTGATTTGCTGCTCTTCTCCAAACTTCGGTC 478
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Qy 539 CAGAATTTCTAGATGATAGCCACTTCAAAATTTGGAGTCTGCTTTGCTTCTCTTGT 598
Db 595 GTGAATTTCCCTGATATGATCAGTTTCTCAATCTTGAAGCTCTCTCTATCAGATTTGAC 654
Qy 599 GCAGAGATGTTCTTTTACAGCGGAGACTGGCAATCCAGTGAATACAGGCTATGTTT 658
Db 655 CAAAGGAATGTTTACCCTGGAG--GAGAGACTGCTGGAGACATGGGAAACTGAGAC 711
Qy 659 ATGCAATATCTAGATGCGGCTGATGTTAATCTGAAAGAAAGAACTGAATTTAAAGGGA 718
Db 712 AGATAATTCAAAGAGAGGAGAAATTTCTGATCAAGAAAGAAAGAAAGCTGACTTTTCCACA 771
Qy 719 GAGATTTGGTACAGGATCTTTGGTAGGCTCGTCAAGGTTTCA-----GTAGAAC 766
Db 772 AAGACATTTATCAGGACTCAACCGGTTTGAAGGCAAAAGGAGAGCAGATGAATA 831
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Db 832 GTGCTGTTATTCGCAAGAAATGAGAAATCAGGTGCGATTTTCTCATCTGCTGCGGTATCA 891
Qy 827 CTATGACAGAACTACTTGGCGATGAGAGCAACTAATGAAACTATACAGTCAAAACAATACA 886
Db 892 AGTTTATGAGAACTCTTATCAGATGATTTCCAACTTTGACAGTTTGAATGACTACTTTT 951
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Db 1072 CCGCTCAAGGACAAAGACTGTTAACCAGTGAATTAAGCAGCCTCTCATGATAAGAACA 1131
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Qy 1127 ATTTGAGGAGCAT---CTGAAAGAAATTTAGATATTGAGCGCTGACACACAATCTTG 1183
Db 1192 CTTTACAGAAGATTTTACTGTCGATTTCCAGATCTTAACCGACTTCCAGAAAGTTTC 1251
Qy 1184 AGAGGAAAGAGCCGATTTAGTGCAGTTGTAAACTCTATCAGTCAAGTACAGAGTAC 1243
Db 1252 AAAGACAGACGAACTTTCAAGATTTGTTACCGACTCTATCAGGATTAATAATCACTAC 1311
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Db 1312 CTAATGTTATACAGGCTCTGGAAACATGAAGGAAACACCCAGAAATTTTGTGGGAG 1371
Qy 1304 GGTATATTGATTTCTAGAGAAATGGAGTGAATCACTGAAATAGTTTCAATAGGTC 1363
Db 1372 TTTTGTGACTCTCTTACTGA-----TCTTCTGCTGACTTCTCCAGTTTCAGGAA 1425
Qy 1364 TTGTGGAACCTTCTGTTGACCTTGTATCACTTGAAGATGGAGAAATACATGATTTCTTCTG 1423
Db 1426 TGATAGAAACAACTTTAGATATGATCAGGTGGAAACCAATGAATTTCTTGTAAACCTT 1485
Qy 1424 CATATGACCCAAATTTATCTGCTCTGAGGATGAGCAAGAGACATTTGGAGCGCAAAATTC 1483
Db 1486 CATTTGATCTTATCTCAGTGAATTTAGAGAAATAATGAATGACTTTGAAAGAGATGC 1545

1484 ATAAATTGACAAACAACTGCAATGATCTTCTGATCTACCTATTGATAAGTCACTTAAC 1543
Db |||||
1546 AGTCAACATTAAATAGTCGAGCCAGAGACTTGGCTTGGACCTTGCACACAGATTAAAC 1605
QY |||||
1544 TAGATTAAGAAACAACTTTGGACAGCTCTTCCAGATTACCAAGAAAGAACCAAAAG 1603
Db |||||
1606 TGGATTCCAGTCGACAGTTGGATATTACTTTCGTAACTCTGTAGGAAGAAAAGTCC 1665
QY |||||
1604 TCAGGAAGCAGCTAAATCTCTACATGTTCTCGAAACAGTAAAGTGGGTAAAGT 1663
Db |||||
1666 TTCTGTA-----CAATAAACTTTAGTACTGTAGATATCCAGAAAGATGGTAAAT 1719
QY |||||
1664 TCACCTATCAAACTCAAACTAGGAGATCAGTTCCAGAAAGATTGTAGAGGAGTACA 1723
Db |||||
1720 TTACCAACAGCAATTCCTTTAAATGAAGATATACCAAAATATAACAGATATG 1779
QY |||||
1724 AAAGCTGTGAGAAAGATTTGGTAGCTGCTGTAGTTCAACAGCTGGAGTTTCCGAGG 1783
Db |||||
1780 AAGAAGCCAGGATGCCATTGTTAAAGAAATTTGTCAATATTTCTTCAGGCTATGTAGA 1839
QY |||||
1784 TGTTCAGGTATAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1843
Db |||||
1840 CAATGAGACATCAATGATGTTAGCTCAGCTAGATCTGTTGTCAGCTTTGCTCAG 1899
QY |||||
1844 TGGCTGCCAGTTGCCCACTCCCTACACAAAGACCAATATCAGTCCACAGATACAGGAG 1903
Db |||||
1900 TGTCAATGGAGCCTGTTCCATATGTACGACAGCCATTTGGAGAAAGACAGGAA 1959
QY |||||
1904 ATATATATCTTCAAGGTTAGGATCTTGTGTGAGAGCTCAAGATTGGGTAACTCCA 1963
Db |||||
1960 GAATATATTAAGCAATCCAGGCTGCTGTTGTTGAAGTTCAAGATGAATTTGCAATTA 2019
QY |||||
1964 TTCTTAATCAGCTAGCTAGTTAGGAGAGAGTTGTTTCAGATATATCAGGCCCTA 2023
Db |||||
2020 TTCTTAATGAGCTATCTTGAAGAAATAACAGATGTTCCACATCATTTACTGGCCCA 2079
QY |||||
2024 ACATGGGTGGAAGTGCACCTACATTCGCGAGTTGGTGTGAATGCTCCTGATGGCCCAAG 2083
Db |||||
2080 ATATGGGAGGTAATCAACATATATTCACAACTGGGTGATAGTACTCAITGGCCCAA 2139
QY |||||
2084 TTGGCTGCTTTGTTCCATGTGACATGCTACATTTCTTATCGTGAATGTTATTTGCTC 2143
Db |||||
2140 TTGGGTGTTTGTGCTATGTAGTCAGAGAGTGTCCATTTGTGAGCTGCATCTTAGGCC 2199
QY |||||
2144 GTGTTGGCTGGAGATTGCCAGCTGAGAGGAGTTTCTACTTTTATGCAAGAGATGCTTG 2203
Db |||||
2200 GAGTAGGGCTGGTGACAGTCAATTTGAAGAGTCTCCAGCTTCAAGCTGAAATGTTGG 2259
QY |||||
2204 AGATGCAATCGATCTTTGAAGAGGCTACTGATAGATCAATGATTATAATGATGATGG 2263
Db |||||
2260 AAATGCTTCTATCTCAGTCTGCAACCAAGATTCATTAATATCATAGATGAATGG 2319
QY |||||
2264 GCCGTGGGACATCACTACCATGCTTGGTTGGTTAGCTTGGGCTATTTGTAGACACATG 2323
Db |||||
2320 GAAGAGGAATCTTACCTACGATGATTTGGTTAGCATGGGCTATATCGAATACATTTG 2379
QY |||||
2324 TTGAAGAAATTAAGCACCACAACTTTGTTGGCCTCACTTTTCAGAGCTGACTGCATTAG 2383
Db |||||
2380 CAACAAAGATTTGGTCTTTTGGATGTTGCAACCCATTTTCAGAACTTACTGCTTGG 2439
QY |||||
2384 CCAACAAAGATTTGGATGGAATAAGAAAATGCTGGGATAGCAAAATTTTCATGTTT 2443
Db |||||
2440 CCAATCAG-----ATACCAACTGTTTAATATCTACATGCA 2475
QY |||||
2444 TTGCACACATTCACCTTCTAATCCAGAGCTAACTATGCTTTTACAGGTTCCACCAAGTG 2503
Db |||||
2476 CAGACTCA-----CCACTGAAGAGACCTTAACCTATGCTTTATCAGGTGAAGAAAGTG 2529
QY |||||
2504 CTTGTGATCAGAGTTTGGTATTCATGTTGCTGAATTTGCAATTTTCCACCGAGTGTG 2563
Db |||||
2530 TCTGTGATCAAGTTTGGGATTCATGTTGAGAGCTTGTCTTAATTTCCCTAAGCATGTAA 2589

QY 2564 TGCTCTCTAGAGAAAGGCATCTGAGTTGAGGATTTCTCTCTATTTGCCATTAATTC 2623
Db |||||
2590 TAGAGTGTCTAAACAGAAAGCCCTTGGAACTTTGAGAGGTTTCAGTATATTGGAGAAATCC 2649
QY |||||
2624 CAAATGACATTAAAGAGGAGCTTCCAAACCGAAGAGAGAAATTTGA 2669
Db |||||
2650 AAGGATATGATATCATCTGAAACCCAGCAGCAAGAAGTGTATCTGGA 2695

RESULT 15

US-10-342-887-455
; Sequence 455, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis, and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 455
; LENGTH: 3145
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-455

Query Match 13.9%; Score 420.8; DB 12; Length 3145;
Best Local Similarity 51.3%; Pred. No. 9.6e-107;
Matches 1194; Conservative 0; Mismatches 1072; Indels 60; Gaps 7;

QY 359 ACTGAGAGCTGGTAAAGTGGAAACCCAGGAACTTGGAGTTTGGAGATATCTGT 418
Db |||||
415 ATTGGTATTGGCATTAAGCTTCTCTGCAATCTCTCAGTTTGAAGACATTTCT 474
QY |||||
419 TTGCTAATTAATGAATGCAAAATTCCTGGTGTATGCTCTTCTCCAACTTCGGTC 478
Db |||||
475 TTGTTAAACATGATATGTCAGCTTCCATTGGTGTGGGTGTTAAATGTCGCAGTTG 534
QY |||||
479 AGAATGATGTAAGTTGGCTTAGCTATGTTGATATTAAGAGAGTCTTGGTTAA 538
Db |||||
535 ATGCCACAGACAGTTGGAGTTGGGTATGTTGATTTCCATACAGAGGAACTAGGACTGT 594
QY |||||
539 CAGAAATTTAGATGATAGCCACTTTCACAAATTTGGAGTCTGCTTTGTTGCTCTGTT 598
Db |||||
595 GTGAATTCCTGATTAATGATCAGTTCTTCAATCTTGAGGCTCTCTCATCAGATTGAC 654
QY |||||
599 GCAGAGATGTTGTATACCAGCGAGAGCTGCAAAATCAGTGAATACAGGCTATGTTG 658
Db |||||
655 CAAAGGAATGTTTTACCCTGGAG- - -GAGAGACTGCTGGAGACATGGGAAACTGAGAC 711
QY |||||
659 ATGCAATATCTAGATCGGGCTGATGTTAACTGAAGAAAGAAAACCTGAATTTAAAGGA 718
Db |||||
712 AGATAATTCAGAGGAGGAAATTTCTGATCAGAAAGAAAAGAAAGCTGCTTTCCCAA 771
QY |||||
719 GAGATTTGGTACAGGATCTTGGTAGGCTCTCAGGTTTCA-----GTAGAAC 765
Db |||||
772 AAGACATTTATCAGACCTCAACCGGTTTGTGAAGGCAAAAAGGAGACAGATGAATA 831
QY |||||
767 CTGTTTCAGATTTGGTCTCTGCTGGGTTCGAATGTGATCAGGCGCTTTGGGTGATATCTT 826

Qy	1904	ATATTTACTTGAAGGGGTGAGGACCTCTTGTGTGGAGGCTCAAGATTGGGTTAACTCCA	1963
Db	1960	GAATTATATTAAAGAGCATCCAGGCATGCTTGTGTGAAAGTTCAAGATGAATTCGATTTA	2019
Qy	1964	TTCTTAATGACTGTAGACTAGTTTAGGGGAGAGAGTTGGTTTCAGATTATCACAGGCCCTA	2023
Db	2020	TTCTTAATGACGTATACCTTTGAAAAAGATAAAACAGATGTTCCACATCATTTACTTGGCCCCA	2079
Qy	2024	ACATGGGTGAAAGTCGACCTACATTCGGCAGGTTGGTGTGAATGTCTCATGGCCCCAAG	2083
Db	2080	ATATGGGAGGTAAATCAACATATATTCGACAAACTGGGTGTAGTACTCATGGCCCAA	2139
Qy	2084	TTGGCTCGTTTGTTCGATGTGAACAATTCCTATTCGTGTGATGTATTTTGTCTC	2143
Db	2140	TTGGGTGTTTTGTGCCATGTGTGAGTCAGCAGAAGTCTCCATTGTGGAGTCGATCTTAAGCCC	2199
Qy	2144	GTGTGTGGCGTGTGAGATTGCCAGCTCAGAGGAGTTTCTATCTTTTATGCAAGAGATGCTTG	2203
Db	2200	GAGTAGGGCTGTGTACAGTCAATTTGAAAGGAGTCTCCAGTTTCATGGCTGGAATGTGTG	2259
Qy	2204	AGACTGCATCGATCTTTGAAGGAGCTACTGATAGATCAATGATTATAATATGATGAGTTGG	2263
Db	2260	AACTGCTTCTATCTCCTCAGTCTGCAACCAAGATTCATTAATAATCATAGATGAATTTG	2319
Qy	2264	GCCGTGGGACATCAACTACGATGGCTTTGGTTTGTAGCTTGGGCTATTTGTGACACATTTG	2323
Db	2320	GAAGAGGAACTTCTACTACGATGGATTTGGGTTTAGCATGGGCTATATCAGAATAACATTTG	2379
Qy	2324	TTGAAGAAATTAAGCACCAACATCTTTTGGCCACTCACTTTCATGAGCTGACGTGCATTAG	2383
Db	2380	CAACAAGATGTGTGTGTTTTTGCAATGTTTGCAACCCATTTTCATGAACCTTACTTGCCTTG	2439
Qy	2384	CCAAAGAAGATGGAGACAATGGACATAAGAAAATGCTGGGATAGCAAAATTTTTCATGTTT	2443
Db	2440	CCAAATCAG-----ATACCAACTGTTAATAATCTACATGTCA	2475
Qy	2444	TTGCACACATTTGACCTTCTAATTCGAAGCTAACTATGCTTTTCAAGGTTTCAACCGGTG	2503
Db	2476	CAGCACTCA-----CCACTGAAGAGACCTTAACTATGCTTTATCAGGTGAAGAAAGGTG	2529
Qy	2504	CTTGTGATCAGAGTTTTTGGTATTCATGTTTCTGCAATTTTCGAAATTTTCCACGAGTGTG	2563
Db	2530	TTGTGTATCAAAAGTTTTTGGATTCATGTGTGCAAGCTTGTCTAATTTTCCCTTAAGCATGTAA	2589
Qy	2564	TGGCTCTGCTACAGAAAAGGACTCTGAGTTGGAGGATTTCTCTCTCTATTGTCCATAATTC	2623
Db	2590	TAGAGTGTGCTAAACAGAAGCCCTGGAACTTTGAGGAGTTTCAGTATATTGGGAATCGC	2649
Qy	2624	CAAATGACATTTAAGAGGCAGCTTCAAACCGGAAGAGAAATTTGA	2669
Db	2650	AAGGATATGATATCATGGAACAGAGCAAGAAAGAGTGTATCTGGA	2695

Search completed: April 9, 2004, 09:54:10
Job time : 1026 secs